

60362

From:
Sent:
To:
Subject:

Zeman, Mary
Thursday, February 14, 2002 10:59 AM
STIC-Biotech/ChemLib
Interference search 09/636801

Please search SEQ ID NO: 392 of 09/636801 in pending files and US Patented files only. Paper printout please.

Thank you,
Mary K. Zeman
Examiner, 1631
305-7133
CM1 12A17
mailbox: CM1 12D01

CRFE

Edward Hart
Technical Info. Specialist
STIC/Biotech
CMI 6B02 Tel: 305-9203

Searcher: _____
Phone: _____
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Date Picked Up: 2/15/02
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Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: 1
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST(where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: 02
WWW/Internet: _____
Other (specify): _____

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EXAMINER
WILLIAM P. SHERMAN
JULY 1988
103-010000-1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:19:30 : Search time 15.01 Seconds

(without alignments)
944,412 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASGRQLHSASTQI.....SSFAISWALPLSPYLMK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 227860 seqs, 45875782 residues

Total number of hits satisfying chosen parameters: 227860

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/1/paa/PCN_NEW_COMB.pep:*
2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1574	100.0	309	6 US-10-010-742-209	Sequence 209, App
2	1431	90.9	282	5 US-09-877-065-8	Sequence 291, App
3	1431	90.9	282	5 US-09-989-723-291	Sequence 291, App
4	1431	90.9	282	5 US-09-989-724-291	Sequence 291, App
5	1431	90.9	282	5 US-09-989-730-291	Sequence 291, App
6	1431	90.9	282	5 US-09-990-436-291	Sequence 291, App
7	1431	90.9	282	5 US-09-989-444-291	Sequence 291, App
8	1431	90.9	282	5 US-09-989-721-291	Sequence 291, App
9	1431	90.9	282	5 US-09-989-722-291	Sequence 291, App
10	1431	90.9	282	5 US-09-989-725-291	Sequence 291, App
11	1431	90.9	282	5 US-09-989-726-291	Sequence 291, App
12	1431	90.9	282	5 US-09-989-727-291	Sequence 291, App
13	1431	90.9	282	5 US-09-989-728-291	Sequence 291, App
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18	1431	90.9	282	5 US-09-990-438-291	Sequence 291, App
19	1431	90.9	282	5 US-09-990-440-291	Sequence 291, App
20	1431	90.9	282	5 US-09-990-441-291	Sequence 291, App
21	1431	90.9	282	5 US-09-989-379-291	Sequence 291, App
22	1431	90.9	282	5 US-09-989-735-291	Sequence 291, App
23	1431	90.9	282	5 US-09-990-439-291	Sequence 291, App
24	1431	90.9	282	5 US-09-990-562-291	Sequence 291, App
25	1431	90.9	282	5 US-09-997-349-291	Sequence 291, App
26	1431	90.9	282	5 US-09-997-542-291	Sequence 291, App

27	1431	90.9	282	5 US-09-997-585-291	Sequence 291, App
28	1431	90.9	282	5 US-09-989-862-291	Sequence 291, App
29	1431	90.9	282	5 US-09-990-427-291	Sequence 291, App
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35	1431	90.9	282	5 US-09-993-604-291	Sequence 291, App
36	1431	90.9	282	5 US-09-994-054-291	Sequence 291, App
37	1431	90.9	282	5 US-09-993-748-291	Sequence 291, App
38	1431	90.9	282	5 US-09-997-601-291	Sequence 291, App
39	1431	90.9	282	5 US-09-997-653-291	Sequence 291, App
40	1431	90.9	282	5 US-09-991-181-291	Sequence 291, App
41	1431	90.9	282	5 US-09-991-854-291	Sequence 291, App
42	1431	90.9	282	5 US-09-992-521-291	Sequence 291, App
43	1431	90.9	282	5 US-09-992-598-291	Sequence 291, App
44	1431	90.9	282	5 US-09-993-469-291	Sequence 291, App
45	1431	90.9	282	5 US-09-993-469-291	Sequence 291, App

ALIGNMENTS

RESULT 1.
US-10-010-742-209
Sequence 209, Application US/10010742
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jlang, Yungu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
APPLICANT: Harlocker, Susan L.
APPLICANT: Bennington, Angela Ann
APPLICANT: Zehentner, Barbara
APPLICANT: Ranger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C7
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-10-010-742-209
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Best Local Similarity 100.0%; Score 1574; DB 6; Length 309;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 HASAHASGRQLHSASTQIRWEPSPAMASLGQILFWSIIIIIIILACALIIIGFGISG 60
DB 1 HASAHASGRQLHSASTQIRWEPSPAMASLGQILFWSIIIIIIILACALIIIGFGISG 60
QY 61 RHSTIVTTVASAGNIGEGGIIISCFEPDIKLSIDIYIOMLKSGVGLVHEFEKGKELSEQ 120
DB 61 RHSTIVTTVASAGNIGEGGIIISCFEPDIKLSIDIYIOMLKSGVGLVHEFEKGKELSEQ 120
QY 121 DEMFRGRTAVRADQYIVNASLRKNVLTGAGTKYKTIISKGGANLKYTGAFSMP 180
DB 121 DEMFRGRTAVRADQYIVNASLRKNVLTGAGTKYKTIISKGGANLKYTGAFSMP 180
QY 181 EVNDYNASSSELRKREARWEPQPTVVASQVDCANSEVSNISFELNSENVTKVYSV 240
DB 181 EVNDYNASSSELRKREARWEPQPTVVASQVDCANSEVSNISFELNSENVTKVYSV 240

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 PRIOR FILING DATE: 1998-07-07
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 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 9.5e-113;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQLIFWISIIIIIIAGALALIGFGISGRHSITVTVVASAGNIGEDGILSCFEP 87
 Db 1 MASIGQLIFWISIIIIIIAGALALIGFGISGRHSITVTVVASAGNIGEDGILSCFEP 60
 QY 88 DIKISDIVIOMLKEGVYGLVHERKEGKDELSODEMFRGRTAVFADOVIVGNASLRKNV 147
 Db 61 DIKISDIVIOMLKEGVYGLVHERKEGKDELSODEMFRGRTAVFADOVIVGNASLRKNV 120
 QY 148 QLTAGTYKCYITTSKKGANLETKGASMPENVNDYANSSFTLCEAPRMPPOPTVV 207
 Db 121 QLTAGTYKCYITTSKKGANLETKGASMPENVNDYANSSFTLCEAPRMPPOPTVV 180
 QY 208 WASQVDGAMFSEVSNTSFELSENENYTMKVSVLYNTJNNVYSCMTENDIAKATGDIKV 267
 Db 181 WASQVDGAMFSEVSNTSFELSENENYTMKVSVLYNTJNNVYSCMTENDIAKATGDIKV 240
 QY 268 TESIERRSHQLINASKASLCVSSFFAISWALPLSPYLMK 309
 Db 241 TESIERRSHQLINASKASLCVSSFFAISWALPLSPYLMK 282

RESULT 4
 US-09-989-724-291
 ; Sequence 291, Application US/09989724
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC67
CURRENT APPLICATION NUMBER: US/09/989,724
CURRENT FILING DATE: 2001-11-20
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44 PRIOR APPLICATION NUMBER: 60/091978
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46 PRIOR APPLICATION NUMBER: 60/091982
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48 PRIOR APPLICATION NUMBER: 60/092182
49 PRIOR FILING DATE: 1998-07-09
50 PRIOR APPLICATION NUMBER: 60/092472

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Query Match	90.9%;	Score 1431;	DB 5;	Length 282;
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			Indels	0;
			Gaps	0;
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Db	1	MASLQQLFWMSIIIIIIILAGAILIIIFGSLISGRHSITVTYTVASAGNIGEDGILSTCFEP	60	
QY	88	DIKLSDIYIOMLKEEVLGLVHEFKGKDBLSQODEMFRGRTAVFADQYIVGNASLRLKNV	147	
Db	61	DIKLSDIYIOMLKEEVLGLVHEFKGKDBLSQODEMFRGRTAVFADQYIVGNASLRLKNV	120	
QY	148	QLTDAGTKCYIITTSKGGKGNANLEKTKTGAFSMEPVNVDMASSEFLRCAAPRWFPOPTVY	207	
Db	121	QLTDAGTKCYIITTSKGGKGNANLEKTKTGAFSMEPVNVDMASSEFLRCAAPRWFPOPTVY	180	
QY	208	MASQVDQGANFSEVSNTSFELNSEENVTKKVVSVLVNLTINNTYSQCIEMNDIAKATGDIKY	267	
Db	181	MASQVDQGANFSEVSNTSFELNSEENVTKKVVSVLVNLTINNTYSQCIEMNDIAKATGDIKY	240	
QY	268	TESFLKRSHQOLNSKASLGVSSFFAIIISWALLPSPIYMLK	309	

Db 241 TSEIKRSHQLNLSKASLCVSSFFAISNALLPLSPYMLWK 282

RESULT 5
US-09-989-730-291

Sequence 291, Application US/09989730

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Bolstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gunney, Austin L.
 APPLICANT: Kijavrin, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2730PIC69
 FILE REFERENCE: P2730PIC69
 CURRENT FILING DATE: 2001-11-20
 PRIOR APPLICATION NUMBER: 60/049787
 PRIOR FILING DATE: 1997-06-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/065186
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 PRIOR APPLICATION NUMBER: 60/075945
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 PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
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 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
PRIOR APPLICATION NUMBER: 60/092472

Query Match          90.98; Score 1431; DB 5; Length 282;
Best Local Similarity 100.08; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLQILFMSIISITILAGALIIIFGSIISRHSITVTTVASAGNIGEDGIIISCTREP 87
Db 1 MASLQILFMSIISITILAGALIIIFGSIISRHSITVTTVASAGNIGEDGIIISCTREP 60
QY 88 DIKLSDIYIOWLKEGVGLVHFEKRGKDELSEODEMFRGRTAVFADQYIVGNASIRLKNV 147
Db 61 DIKLSDIYIOWLKEGVGLVHFEKRGKDELSEODEMFRGRTAVFADQYIVGNASIRLKNV 120
QY 148 QLTDAQYIKCYIITISKKGANLLEKYGAFSMPVEYVNDYNASSETTLRCEADRWEPQPTVV 207
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|||||
Db 121 QLTAGTYKCYIITSKGKGNANLEKTKGAFSMPEVNVVDYNNASSETLRCEADPMFPQPIVV 180
OY 208 WASOVDOGANFSEVSNSEFEINSENVTKKVSVLNTNTINNTSCMIENDIAKAGDIDKV 267
Db 181 WASOVDOGANFSEVSNSEFEINSENVTKKVSVLNTNTINNTSCMIENDIAKAGDIDKV 240
OY 268 TESEIKRSHQLNSKASLCVSSFFAISMLPLSPYIMLK 309
Db 241 TESEIKRSHQLNSKASLCVSSFFAISMLPLSPYIMLK 282
RESULT 6
US-09-990-436-291
Sequence 291, Application US/09990436
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, Paul J.
APPLICANT: Gruney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089653
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089908
PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089947
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089948

Query Match	90.9%	Score 1431	DB 5	Length 282
Best Local Similarity	100.0%	Pred. No. 9.5e-113		
Matches 282	Conservative 0	Mismatches 0	Indels 0	Gaps 0

PRIOR APPLICATION NUMBER: 60/083342
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106

[illegible]

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; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092472
Query Match          90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWSIIIIIIILGAILIIFGISGRHSITVTYTVASAGNIGEDILSCFEP 87
DB 1 MASLGQILFWSIIIIIIILGAILIIFGISGRHSITVTYTVASAGNIGEDILSCFEP 60
QY 88 DILSDIVIQMLKEGVGLVHERKEGDELSEODEMRGTAFAPOVITYGNASLRKNV 147
DB 61 DILSDIVIQMLKEGVGLVHERKEGDELSEODEMRGTAFAPOVITYGNASLRKNV 120
QY 148 QLTDACTYKCYIITTSKGNANLEYKTGAFSMEPVNVYVASSETLRCAPRPFPOPTV 207
DB 121 QLTDACTYKCYIITTSKGNANLEYKTGAFSMEPVNVYVASSETLRCAPRPFPOPTV 180
QY 208 MASQVQGANFSEVSNITSEFLNSENVTMKVSVLYNVTINNTYSCEMIENDIAKATGDIKY 267
DB 181 MASQVQGANFSEVSNITSEFLNSENVTMKVSVLYNVTINNTYSCEMIENDIAKATGDIKY 240
QY 268 TESEIKRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 309
DB 241 TESEIKRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 282

RESULT      8
US-09-989-721-291
; Sequence 291, Application US/09989721
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC55
; CURRENT APPLICATION NUMBER: US/09/989,721
; CURRENT FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/049787
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; PRIOR APPLICATION NUMBER: 60/075945
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; PRIOR APPLICATION NUMBER: 60/089538
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: PRIOR FILING DATE: 1998-07-01
: PRIOR APPLICATION NUMBER: 60/091478
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091544
: PRIOR FILING DATE: 1998-07-01

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: PRIOR APPLICATION NUMBER: 60/091519
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091626
: PRIOR FILING DATE: 1998-07-02
: PRIOR APPLICATION NUMBER: 60/091633
: PRIOR FILING DATE: 1998-07-02
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: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/091982
: PRIOR FILING DATE: 1998-07-07
: PRIOR APPLICATION NUMBER: 60/092182
: PRIOR FILING DATE: 1998-07-09
: PRIOR APPLICATION NUMBER: 60/092472

Query Match          90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9, 5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQILFWSTISITITILAGAILIGFGISGRHSITVTYVASAGNIGEDGILSCTEP 87
DB 1 MASIGQILFWSTISITITILAGAILIGFGISGRHSITVTYVASAGNIGEDGILSCTEP 60

QY 88 DIKLSDIYIOWLKEGVGLVHEFEKGDLSODEMFRGRTAVFADQYVGNASIRLKNV 147
DB 61 DIKLSDIYIOWLKEGVGLVHEFEKGDLSODEMFRGRTAVFADQYVGNASIRLKNV 120

QY 148 QLTDAITYKCYITITSKGGANLXKTAFSKPEVNVNDYNASSETLRCEAPRFPQPIVY 207
DB 121 QLTDAITYKCYITITSKGGANLXKTAFSKPEVNVNDYNASSETLRCEAPRFPQPIVY 180

QY 208 WASQVDGAFNSEVNTSEFELNSENVTMKVSVLYNVNTINNYSGMTENDIAKATGDIKV 267
DB 181 WASQVDGAFNSEVNTSEFELNSENVTMKVSVLYNVNTINNYSGMTENDIAKATGDIKV 240

QY 268 TESEIKRRSHQLNSKASLCVSSFFAISMALLPLSPYLMUK 309
DB 241 TESEIKRRSHQLNSKASLCVSSFFAISMALLPLSPYLMUK 282

RESULT 9
US-09-989-722-291
: Sequence 291, Application US/09989722
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gerlitsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Kiljavin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secretd and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C63
: CURRENT APPLICATION NUMBER: US/09/989,722
: CURRENT FILING DATE: 2001-11-19
: PRIOR APPLICATION NUMBER: 60/049787

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;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/090863
;; PRIOR FILING DATE: 1998-06-26
;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091519
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091626
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091633
;; PRIOR FILING DATE: 1998-07-02
;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASIGQLFWSIIITIIILACALIIIGFISGRHSITVTVAASAGNIGEGCIISCTPEP 87
DB 1 MASIGQLFWSIIITIIILACALIIIGFISGRHSITVTVAASAGNIGEGCIISCTPEP 60
QY 88 DIKLSDIVIOWLKEGVLCGLVHEFEKGEKDELSEODEMFGRPTAVFADQYIVGNASIRLKNV 147
DB 61 DIKLSDIVIOWLKEGVLCGLVHEFEKGEKDELSEODEMFGRPTAVFADQYIVGNASIRLKNV 120
QY 148 QLTDAGYTKCYIITSKGNANLEYKYGAFSMPEVNDVYNASSETLRCEAPRWFQPTIV 207
DB 121 QLTDAGYTKCYIITSKGNANLEYKYGAFSMPEVNDVYNASSETLRCEAPRWFQPTIV 180
QY 208 WASOVDOGANSEVSNISFELNSENVTMKVSVLYNVTINNTYSMIENDIAKATGDIKV 267
DB 181 WASOVDOGANSEVSNISFELNSENVTMKVSVLYNVTINNTYSMIENDIAKATGDIKV 240
QY 268 TSEIKRSHQLNSKASLCVSSFPFAISWALLPLSPYLMUK 309
DB 241 TSEIKRSHQLNSKASLCVSSFPFAISWALLPLSPYLMUK 282

RESULT 10
US-09-989-725-291
;; Sequence 291, Application US/09989725
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Eaton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavlin, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Paoni, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Watanabe, Colin K.

;; APPLICANT: Williams, P. Mickey
;; APPLICANT: Wood, William I.
;; APPLICANT: Zhang, Zemin
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
;; FILE REFERENCE: P2730P1C71
;; CURRENT APPLICATION NUMBER: US/09/989,725
;; PRIOR FILING DATE: 2001-11-20
;; PRIOR APPLICATION NUMBER: 60/049787
;; PRIOR FILING DATE: 1997-06-16
;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
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PRIOR FILING DATE: 1998-06-10
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 PRIOR APPLICATION NUMBER: 60/091978
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/091982
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09
 PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
 Best Local Similarity 100.0%; Pred. No. 9.5e-113;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGILFWSTISITIIITAGAILIGISGRHSITVTVYASAGNTEEDGILSTFEP 87
 DB 1 MASLGILFWSTISITIIITAGAILIGISGRHSITVTVYASAGNTEEDGILSTFEP 60
 QY 88 DIKLSDIVIQLKEGVLGLVHEFEKSKDELSEDEMFRRGTAVFADQVIVGNASLRKVV 147
 DB 61 DIKLSDIVIQLKEGVLGLVHEFEKSKDELSEDEMFRRGTAVFADQVIVGNASLRKVV 120
 QY 148 QLTDACTYKCYIITSSKGNANLEKVTGAFSPMEVVDYNASSETLRCEAPRMPQPTVV 207
 DB 121 QLTDACTYKCYIITSSKGNANLEKVTGAFSPMEVVDYNASSETLRCEAPRMPQPTVV 180
 QY 208 MASOVDOGANFSEVSWTSELSSENVTKMVSIVLVNTINNTYSCHIENDIAKATGDIV 267
 DB 181 MASOVDOGANFSEVSWTSELSSENVTKMVSIVLVNTINNTYSCHIENDIAKATGDIV 240
 QY 268 TESEIKRRSHLOLINSKASLCVSPFAISWALLPLSPYLMK 309
 DB 241 TESEIKRRSHLOLINSKASLCVSPFAISWALLPLSPYLMK 282

RESULT 11
 US-09-989-726-291
 ; Sequence 291, Application US/09989726
 ; GENERAL INFORMATION:
 ; APPLICANT: Ashkenazi, Avi J.
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Botstein, David
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Eaton, Dan L.
 ; APPLICANT: Ferrara, Napoleone
 ; APPLICANT: Fong, Sherman
 ; APPLICANT: Getzler, Hanspeter
 ; APPLICANT: Gerlitsen, Mary E.
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.
APPLICANT: Kijavira, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/075945
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? PRIOR FILING DATE: 1998-07-09
? PRIOR APPLICATION NUMBER: 60/092472
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* Query Match          90.9%; Score 1431; DB 5; Length 282;
  Best Local Similarity 100.0%; Pred No. 9.5e-113;
  Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
?
QY 28 MASLQILFWSIITIIIIAGAILIIGFISGRHSITVTYVASAGNIGEDGILSCTFEP 87
DB 1 MASLQILFWSIITIIIIAGAILIIGFISGRHSITVTYVASAGNIGEDGILSCTFEP 60
QY 88 DIKLSIDIVQWLKEGYLGIVHEFKESKDELSEODEMFRGRTAVFADQVIVGNASLRLKNV 147
DB 61 DIKLSIDIVQWLKEGYLGIVHEFKESKDELSEODEMFRGRTAVFADQVIVGNASLRLKNV 120
QY 148 QLTDAQTYCYIITISGKGNANLEKKTGAFSMEPVVVDYNASSETLRCEAPRMEPQPTV 207
DB 121 QLTDAQTYCYIITISGKGNANLEKKTGAFSMEPVVVDYNASSETLRCEAPRMEPQPTV 180
QY 208 WASQVDOGANFSEVNTSELSSENVYTMKVSVLYNVITNTNTYSCMIENDIKATGDIKV 267
DB 181 WASQVDOGANFSEVNTSELSSENVYTMKVSVLYNVITNTNTYSCMIENDIKATGDIKV 240
QY 268 TSESEIKRSHLOLLNSKASLCVSSFFAISMALLPLSPYIMLK 309
DB 241 TSESEIKRSHLOLLNSKASLCVSSFFAISMALLPLSPYIMLK 282
?
RESULT 12
US-09-989-727-291
? SEQUENCE 291, Application US/09989727
? GENERAL INFORMATION:
? APPLICANT: Ashkenazi, Avi J.
? APPLICANT: Baker, Kevin P.
? APPLICANT: Botstein, David
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? APPLICANT: Desnoyers, Luc
? APPLICANT: Eaton, Dan L.
? APPLICANT: Ferrara, Napoleone
? APPLICANT: Fong, Sherman
? APPLICANT: Gerber, Hanspeter
? APPLICANT: Gerltsen, Mary E.
? APPLICANT: Goddard, Audrey
? APPLICANT: Godowski, Paul J.
? APPLICANT: Grimaldi, J. Christopher
? APPLICANT: Gurney, Austin L.
? APPLICANT: Kijavlin, Ivar J.
? APPLICANT: Napier, Mary A.
? APPLICANT: Pan, James
? APPLICANT: Paoni, Nicholas F.
? APPLICANT: Roy, Margaret Ann
? APPLICANT: Stewart, Timothy A.
? APPLICANT: Tumas, Daniel
? APPLICANT: Watanabe, Collin K.
? APPLICANT: Williams, P. Mickey
? APPLICANT: Wood, William I.
? APPLICANT: Zhang, Zemin
? TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
? FILE REFERENCE: P2730PIC65
? CURRENT APPLICATION NUMBER: US/09/989,727
? PRIOR FILING DATE: 2001-11-19
? PRIOR APPLICATION NUMBER: 60/049787
? PRIOR FILING DATE: 1997-06-16
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;; PRIOR FILING DATE: 1998-07-09
;; PRIOR APPLICATION NUMBER: 60/092472

Query Match 90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.3e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 28 MASLGOILFWSTIISIIILAGAILIGISGRSITVTVASAGNIGEDDILSCTEEP 87
Db 1 MASLGOILFWSTIISIIILAGAILIGISGRSITVTVASAGNIGEDDILSCTEEP 60
Oy 88 DIKLSDIYIOWLKEGVGLVHEFKGKDELSEBODEMFGRTAVFADQYIVGNASLRKNV 147
Db 61 DIKLSDIYIOWLKEGVGLVHEFKGKDELSEBODEMFGRTAVFADQYIVGNASLRKNV 120
Oy 148 QLTDAGYTKCYITTSKGNANLEKTKGAFSPPEVNVDMASSETLRCEAPMFPQPIVY 207
Db 121 QLTDAGYTKCYITTSKGNANLEKTKGAFSPPEVNVDMASSETLRCEAPMFPQPIVY 180
Oy 208 WASOVDGAFNESEVNTSPELSENVTAKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
Db 181 WASOVDGAFNESEVNTSPELSENVTAKVSVLYNVTINNTYSCMIENDIAKATGDIKV 240
Oy 268 TESEIKRSHLOLNSKASLVCVSPFAISWALLPLSPYLMK 309
Db 241 TESEIKRSHLOLNSKASLVCVSPFAISWALLPLSPYLMK 282

RESULT 13
US-09-989-728-291
Sequence 291, Application US/09989728
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C72
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/090349

Query Match	90.9%	Score 1431	DB 5	Length 282
Best Local Similarity	100.0%	Pred. No. 9.5e-113		
Matches 282	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	28	MASIGQILFWISIIIIIIAGAILIIIGPGISGRHSITVTVTVAASAGNIGEDGILSTPEP	87	
DB	1	MASIGQILFWISIIIIIIAGAILIIIGPGISGRHSITVTVTVAASAGNIGEDGILSTPEP	60	
QY	88	DIKLSIDIYIOMLKEGVGLVJHFEKSGKDELSPQDEMFRCRTAFVFPDQVIVGNASLRKLV	147	
DB	61	DIKLSIDIYIOMLKEGVGLVJHFEKSGKDELSPQDEMFRCRTAFVFPDQVIVGNASLRKLV	120	
QY	148	QLTADGATKCYIIITSKGGNANLEKKTGAFSMPEVENVVOYNASSETLRCAAPWFPQPIV	207	

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Db      121 QLTDAAGYKKCIILSKKGNANLEIKGCARSMPEVANDYVASSETLRCAPRRFPPQPTV 180
QY      208 WASOVDOGANEFSEVSNTPFELINSENVTKAVSVLYNVNTINNTYSCTMIENDIAKATGDIKY 267
Db      181 WASOVDOGANEFSEVSNTPFELINSENVTKAVSVLYNVNTINNTYSCTMIENDIAKATGDIKY 240
QY      268 TESIKRRSHQLLNKSKASLCVSEFAISWALLPLSPYMLK 309
Db      241 TESEIKRRSHQLLNKSKASLCVSEFAISWALLPLSPYMLK 282

RESULT 14
US-09-989-731-291
: Sequence 291, Application US/09989731
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Botstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Gertlisen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavlin, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: TITLE OF INVENTION: Acids Encoding the Same
: FILE REFERENCE: P2730P1C70
: CURRENT APPLICATION NUMBER: US/09/989,731
: CURRENT FILING DATE: 2001-11-20
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
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Query Match 90.9%; Score 1431; DB 5; Length 282;
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Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PRIOR APPLICATION NUMBER: 60/087607	
PRIOR FILING DATE: 1998-06-02	
PRIOR APPLICATION NUMBER: 60/087609	
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PRIOR APPLICATION NUMBER: 60/087755	
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PRIOR APPLICATION NUMBER:	60/089908
PRIOR FILING DATE:	1998-06-18
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PRIOR APPLICATION NUMBER:	60/091633
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PRIOR APPLICATION NUMBER:	60/091978
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PRIOR FILING DATE:	1998-07-07

; PRIOR APPLICATION NUMBER: 60/092182
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 ; PRIOR FILING DATE: 1998-07-09
 ;
 ; PRIOR APPLICATION NUMBER: 60/092472
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Query Match      90.9%; Score 1431; DB 5; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.5e-113;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 1 MASLGGILEWMSIISIIIIILAGALALILGIGISGRHSITVTTVASAGNIGEDGILSTFEP 60

Dc 61 DIKLSDIYIQWLKEGVLGVHEFEKGDELSEODEMFRGRRTAVFADQVIYNASLRILKNV 120C
Qy 88 DIKLSDIYIQWLKEGVLGVHEFEKGDELSEODEMFRGRRTAVFADQVIYNASLRILKNV 147R

Dy 148 QLTDAGYKCYIITSKGKANLEYKTGAFSMEVNVYNASSETLRCEAFRWFPQPTVV 207
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Db 121 QLTDAGYKCYIITSKGKANLEYKTGAFSMEVNVYNASSETLRCEAFRWFPQPTVV 180

Qy 208 MASQVDGAGNFSEVNTSEFENSENTYMKVSVLYNTVNTNTYSCMIENDIAKATGDIKV 267
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 Db 181 MASQVDGAGNFSEVNTSEFENSENTYMKVSVLYNTVNTNTYSCMIENDIAKATGDIKV 240

Dy 268 TESIIKRRSHLQLNLSKASLCVSSFFAISWMLLPSPYLMIK 309
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Db 241 TESIIKRSHLQNLNSKASLCVSSFFAISWMLPLPSYLMIK 282

Search completed: February 15, 2002, 14:22:46
Job time: 196 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2002, 14:18:55 : Search time 12.65 Seconds

(without alignments)
549.085 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574
Sequence: 1 HASAHASGRQLHSASTQI.....SSFFAISMALPLSPYLMK 309

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 212252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: Issued_Patents_AA:*
2: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
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6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.5	13.8	540	2	US-08-724-394A-4
2	212.5	13.5	610	2	US-08-724-394A-5
3	211.5	13.4	589	2	US-08-724-394A-1
4	207.5	13.2	342	2	US-08-724-394A-6
5	186	11.8	581	2	US-08-724-394A-2
6	183	11.6	581	2	US-08-724-394A-3
7	147.5	9.4	323	5	PCT-US94-09642-2
8	147.5	9.4	329	2	US-08-456-104-2
9	147.5	9.4	329	2	US-08-101-624-2
10	147.5	9.4	329	3	US-08-479-744A-2
11	147.5	9.4	329	4	US-08-280-757B-2
12	147.5	9.4	329	4	US-08-205-697A-23
13	147.5	9.4	329	4	US-08-702-525-23
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15	144	9.1	247	5	PCT-US94-10257A-2
16	143.5	9.1	309	2	US-08-456-104-4
17	143.5	9.1	309	3	US-08-479-744A-23
18	143.5	9.1	309	4	US-08-280-757B-23
19	143.5	9.1	309	4	US-08-205-697A-21
20	143.5	9.1	309	4	US-08-702-525-21
21	143.5	9.1	309	5	PCT-US95-02576-21
22	143.5	9.1	314	4	US-08-205-697A-13
23	143.5	9.1	314	4	US-08-702-525-13
24	143.5	9.1	314	4	US-08-702-525-13
25	132	8.4	478	5	PCT-US95-02576-13
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27	132	8.4	868	1	US-08-374-834-1

28	132	8.4	868	2	US-08-644-271-1	Sequence 1, Appl
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30	128	8.1	365	4	US-08-928-383B-23	Sequence 23, Appl
31	128	8.1	365	4	US-08-928-383B-24	Sequence 24, Appl
32	127	8.1	946	5	PCT-US95-08493-13	Sequence 15, Appl
33	124.5	7.9	208	3	US-08-630-172-15	Sequence 15, Appl
34	124.5	7.9	208	4	US-08-375-419-15	Sequence 15, Appl
35	124	7.9	306	2	US-08-147-772-4	Sequence 4, Appl
36	124	7.9	306	2	US-08-456-104-8	Sequence 8, Appl
37	124	7.9	306	2	US-08-101-624-25	Sequence 25, Appl
38	124	7.9	306	3	US-08-153-262-4	Sequence 4, Appl
39	124	7.9	306	3	US-08-479-744A-31	Sequence 31, Appl
40	124	7.9	306	4	US-08-280-757B-31	Sequence 31, Appl
41	124	7.9	306	4	US-09-159-135-4	Sequence 4, Appl
42	124	7.9	306	4	US-08-205-697A-17	Sequence 17, Appl
43	124	7.9	306	4	US-08-702-525-17	Sequence 17, Appl
44	124	7.9	306	5	PCT-US95-02576-17	Sequence 17, Appl
45	124	7.9	320	4	US-08-205-697A-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-724-394A-4
: Sequence 4, Application US/08724394A
: Patent No. 5872237
: GENERAL INFORMATION:
: APPLICANT: Feder, John N.
: APPLICANT: Kronmal, Gregory S.
: APPLICANT: Laufer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchinashi, Zenta
: APPLICANT: Wolff, Roger K.
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
: TITLE OF INVENTION: Sequences and Antibodies Thereto
: NUMBER OF SEQUENCES: 31
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Fitts, Renee A. 35,136
: REGISTRATION NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
: INFORMATION FOR SEQ ID NO: 4:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 540 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..540
: OTHER INFORMATION: /note= "BTF5"
US-08-724-394A-4

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Query Match 13.8% Score 217.5 DB 2 Length 540:
Best Local Similarity 25.6% Pred. No. 7.3e-14:
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QY 178 SMEPEVNDV--YNASSETLRCEAPRMPFPQPTVVAASQDOGANFSEVSNTSELSENVY 234
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QY 235 MKVV--SVLYNVTINNTYSCHENDI--AKATGDKATVE 269
      ||:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 204 LYAAVASVIMRGSSGEVSCITRSSLGLLEKTAASISAD 242

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RESULT 2
US-08-724-

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: Sequence 5, Application US/08724394A
: Patent No. 5872237
:
: GENERAL INFORMATION:
:
: APPLICANT: Feder, John N.
: APPLICANT: Krommal, Gregory S.
: APPLICANT: Lauer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchibashi, Zenta
: APPLICANT: Wolff, Roger K.
:
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
:
: TITLE OF INVENTION: Sequences and Antibodies Thereto
:
: NUMBER OF SEQUENCES: 31
:
: CORRESPONDENCE ADDRESS:
:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
:
: STREET: Two Embarcadero Center, 8th floor
:
: CITY: San Francisco
:
: STATE: CA
:
: COUNTRY: USA
:
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
:
: MEDIUM TYPE: Floppy disk
:
: COMPUTER: IBM PC compatible
:
: OPERATING SYSTEM: PC-DOS/MS-DOS
:
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
:
: APPLICATION NUMBER: US/08/724,394A
:
: FILING DATE: 01-OCT-1996
:
: CLASSIFICATION: 536
:
: ATTORNEY/AGENT INFORMATION:
:
: NAME: Filts, Renee A.
:
: REGISTRATION NUMBER: 35,136
:
: REFERENCE/DOCKET NUMBER: 017957-000100
:
: TELECOMMUNICATION INFORMATION:
:
: TELEPHONE: 415-576-0200
:
: TELEFAX: 415-576-0300
:
: INFORMATION FOR SEQ ID NO: 5:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 610 amino acids
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: TYPE: amino acid
:
: STRANDEDNESS: not relevant
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: TOPOLOGY: not relevant
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: MOLECULE TYPE: peptide
:
: FEATURE:
:
: NAME/KEY: Region
:
: LOCATION: 1..610
:
: OTHER INFORMATION: /note= "BTF3"
:
: US-08-724-394A-5

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Db	VGEDIDLPCHLEPPTSAETMELRWVSSSLRQVVAVYADQEKVEDQSAARYBRTSILRRG	106			
OY	135 VIVGASLRRLKNVOLTDJGTGYKCYLITTSKGKNALERTKAFSMAPEVVD---YNASE	191			
Db	107 ITAGCAALRIHNVYASDSBGKTLCTFQDDGFYEKALVELKVALGLG--SDLHIKEYGDEDGI	165			
OY	192 TLRCAPRMFDPOPIVVAASOVDOGANFSEVSNTSFELSSENTMKRV--SVLYANTINNT	249			
Db	166 HLECKSTGMYPQLKMSD--TKGENIPAV--EAPVYADQGLVAVAASYIMRSSSGG	220			
OY	250 YSCMIENDI--AKATGDIKYTE	269			
Db	221 VSCIIRNSLLGLEKTASTISIA	242			

RESULT 3

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US-08-724-394A-1
: Sequence 1A, Application US/08/24394A
: Patent No. 5872237
:
: GENERAL INFORMATION:
:
: APPLICANT: Feder, John N.
: APPLICANT: Krommal, Gregory S.
: APPLICANT: Laufer, Peter M.
: APPLICANT: Ruddy, David A.
: APPLICANT: Thomas, Winston
: APPLICANT: Tsuchihashi, Zenta
: APPLICANT: Wolff, Roger K.
:
: TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e
: NUMBER OF SEQUENCES: 31
:
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
: STREET: Two Embarcadero Center, 8th Floor
: CITY: San Francisco
: STATE: CA
: COUNTRY: USA
: ZIP: 94111-3834
:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/724,394A
: FILING DATE: 01-OCT-1996
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Filts, Renee A.
: REGISTRATION NUMBER: 35,136
: REFERENCE/DOCKET NUMBER: 017957-000100
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-576-0200
: TELEFAX: 415-576-0300
:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 589 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: not relevant
: MOLECULE TYPE: peptide
: FEATURE:
: NAME/KEY: Region
: LOCATION: 1..589
: OTHER INFORMATION: /note="Br"
:
: US-08-724-394A-1

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Query Match      13.24; Score 207.5; DB 2; Length 342;
Best Local Similarity 26.18; Pred. No. 3.7e-13;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

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Db 47 VGEDADLPCHLEPPTMSAETMELKWSSSLRQVYVNYADGKEVEDGQSAIPRGRTSLRNG 106
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 135 VIVGNASIRLKNVQLTDAGTYKCIITTSKKGKNANLEKTKGAF-SMPEYNV-DYNASSET 192
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Db 167 LECRSTGWYRPOPQIOWMSNAKGENTIPAVAPAPVYADGVGLYEVA-----ASV 211
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QY 241 LYNTVINTNTYSQMIENDI-AKATGDIKYTE 269
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
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RESULT 5
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Sequence 2, Application US/08724394A
Patent No. 5872237
GENERAL INFORMATION:
APPLICANT: Feder, John N.
APPLICANT: Krommal, Gregory S.
APPLICANT: Lauer, Peter M.
APPLICANT: Ruddy, David A.
APPLICANT: Thomas, Winston
APPLICANT: Tsuchihashi, Zenta
APPLICANT: Wolff, Roger K.
TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
TITLE OF INVENTION: Sequences and Antibodies Thereof
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREM LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,394A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 017957-000100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0300
TELEFAX: 415-576-0200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 581 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Region
LOCATION: 1..581
OTHER INFORMATION: /note= "BFP1"
US-08-724-394A-2

```

Query Match 11.8%; Score 186; DB 2; Length 581;
 Best Local Similarity 23.6%; Pred. No. 1.4e-10;
 Matches 52; Conservative 41; Mismatches 115; Indels 12; Gaps 5;

QY 42 IITLILGAVLILIGFGISGRHSITVTVASAGNIGEDGLSCFFEPDIKSDIVIQWLKE 101
 Db 19 LLLLLSLCAL-----VSAQFIVGPPDPLATVGEHTTLRCHLSPKNAEDMEVRFERS 73
 QY 102 GVLGVHEFEKGDDELSEODEMFRGTAVFADQIVGNASLRKNVQLTDAGTYKCYIT 161
 Db 74 QFSPAVAVYKGRRETEDEQMEYRGRTTFVSKISRGVALYHNITAQENGITRCFQE 133
 QY 162 SKKGNANLE-YKTGAFSMEPVNV-DYMASSEFLRCEAPRWPQPTVYMASQVDQGA-NF 218
 Db 134 GRGYDAIILHLVYAGLSKPLISMRCHEGDIRLECISRGWYPRPLTWMDPYGVAPAL 193
 QY 219 SEVSNTSFELSENVTMKVSVLYNTVINTYSCMIENDI 258
 Db 194 KEVSWP-----DADGLFMVTTAVIIRDKSVRNMSCSINNTL 229

RESULT 6

US-08-724-394A-3

Sequence 3, Application US/08724394A

Patent No. 5872237

GENERAL INFORMATION:

APPLICANT: Feder, John N.

APPLICANT: Kronmal, Gregory S.

APPLICANT: Lauer, Peter M.

APPLICANT: Ruddy, David A.

APPLICANT: Thomas, Winston

APPLICANT: Tsuchihashi, Zenta

TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/724,394A

FILING DATE: 01-OCT-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Filts, Renee A.

REGISTRATION NUMBER: 35,136

REFERENCE/DOCKET NUMBER: 01957-000100

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-576-0200

TELEFAX: 415-576-0300

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 581 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: not relevant

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Region

LOCATION: 1..581

OTHER INFORMATION: /note- "BTF2"

US-08-724-394A-3

Query Match 11.6%; Score 183; DB 2; Length 581;
 Best Local Similarity 23.6%; Pred. No. 2.9e-10;
 Matches 59; Conservative 42; Mismatches 113; Indels 36; Gaps 8;

QY 23 EEPSPM-----ASLGOLFMSITSIITIIILAGALALLIGFISGRHSITVTVASAGNI-- 75
 Db 2 EPAALHFSLPASL-----LLLLLLLSLICALV-----SAQFVYVAPAPITLA 45
 QY 76 --GEDGLSCFFEPDIKSDIVIQWLKEGVLVHEFEKGDDELSEODEMFRGTAVFAD 133
 Db 46 MVEENTTLRCHLSPKNAEDMEVRFERSQSPAVFYKGRRETEDEQMEYRGRTTFVSK 105
 QY 134 QVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLE-YKTGAFSMEPVNV-DYMASSE 191
 Db 106 DINRGSAVALYHNITAQENGITRCYFQEGRSYDEAILRLVYAGLSKPLIEIKAQEDGSI 165
 QY 192 TLRCAPRWPQPTVYMASQVDQGANFSEVSNTSFEL---NSENVTKVSVLYNTVIN 248
 Db 166 WLECISGQWYPRPLTWMDPYGVAPALKEVSIADADGLFMVTTAVIIRDKYVR 219
 QY 249 TYSQMIENDI 258
 Db 220 NVSCSVNNTL 229

RESULT 7

PCT-US94-09642-2

Sequence 2, Application PC/TUS9409642

GENERAL INFORMATION:

APPLICANT: Purified Mammalian CTLA-4 Binding

TITLE OF INVENTION: Protein and Related Reagents

NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:

ADDRESSEE: Schering-Plough Corporation, M-3-W

STREET: One Giralda Farms

CITY: Madison

STATE: New Jersey

COUNTRY: USA

ZIP: 07940-1000

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh IIcx

OPERATING SYSTEM: System Software 7.1

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/09642

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/120,606

FILING DATE: 13-SEP-1993

APPLICATION NUMBER: US 08/116,882

FILING DATE: 03-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Blasdale, John H. C.

REGISTRATION NUMBER: 31,895

REFERENCE/DOCKET NUMBER: DX0390K1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-822-7039

TELEFAX: 201-822-7398

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 323 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US94-09642-2

Query Match	9.4%;	Score 147.5;	DB 2;	Length 329;
Best Local Similarity	23.4%;	Pred. No. 5.3e-07;		
Matches 67;	Conservative 43;	Mismatches 109;	Indels 67;	Gaps 13;

MOLECULE TYPE: protein
US-08-280-757B-2

Query Match	9.48;	Score 147.5;	DB 4;	Length 329;
Best Local Similarity	23.48;	Pred No. 5.3e-07;		
Matches 67; Conservative	43;	Mismatches 109;	Indels 67;	Gaps 13;

[illegible]

RESULT 12
US-08-205-697A-23
; Sequence 23, Application US/08205697A
; Patent No. 6310510

GENERAL INFORMATION:
 APPLICANT: Sharpe, Arlene H.
 APPLICANT: Borriello, Francescopaolo
 APPLICANT: Freeman, Gordon J.
 APPLICANT: Nadler, Lee M.
 TITLE OF INVENTION: No. 6218510e1 Forms of T Cell Costimulatory Molecules
 TITLE OF INVENTION: and uses therefor
 NUMBER OF SEQUENCES: 61

ADDRESS: LAHAYE & COCKFIELD
STREET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/205,697M
FILING DATE: 02-Mar-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36 207

REFERENCE/DOCKET NUMBER: BHL-120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid

MOLECULE TYPE: protein
US-08-205-697A-23

Query Match 9.48; Score 147.5; DB 4; Length 329;

Best Local Similarity 23.4%; Pred. No. 5.3e-07;
Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

[illegible]

RESULT 13
US-08-702-525-23
: Sequence 23, Application US/08702525

1. COUNTRY: U.S.A.
 2. APPLICANT: Sharpe, Sharpe
 3. APPLICANT: Borriello, Francescopolo
 4. APPLICANT: Freeman, Gordon
 5. APPLICANT: Nadler, Lee
 6. TITLE OF INVENTION: No. 629460el Forms of T Cell Costimulatory
 7. TITLE OF INVENTION: Molecules and uses therefor
 8. NUMBER OF SEQUENCES: 65
 9. CORRESPONDENCE ADDRESS:
 10. ADDRESSEE: LAHIVE & COCKFIELD
 11. STREET: 28 State Street
 12. CITY: Boston

```

? COUNTRY: USA
? ZIP: 02109-1875
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: ASCII Text
? CURRENT APPLICATION DATA:

```

? FILING DATE: 08-MAR-1994
 ? PRIOR APPLICATION DATA: US 08/205,697
 ? APPLICATION NUMBER: 02-MAR-1994
 ? FILING DATE: 02-MAR-1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Mandacouras, Amy E.
 ? REGISTRATION NUMBER: 36,207
 ? REFERENCE/DOCKET NUMBER: BWT-1120CPS1

TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ. ID NO.: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 329 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-702-525-23

Query Match	9.48;	Score 147.5;	DB 4;	Length 329;
Best Local Similarity	23.48;	Pred. No. 5.3e-07;		
Matches 67;	Conservative 43;	Mismatches 109;	Indels 67;	Gaps 13;

```

QY 50 IALIGFGISGRHSITVTTVASAGNIGEDGILCTF--EPDIKLSDIVIOMLKEGVGLV 107
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 12 ILFVMAFLLSGAAPLKIQAY-----FNETADLPCOFANSQOSISLSELYVMQOENL-VL 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 108 HEFEKGEDELSEODEMFRGTAVFADQVIYGNASLRKLNQVLDAQYKCYITTSKGG- 166
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 66 NEVYLKREKEDSVHSHKMGTSFSDS-----SWTLRLHNIQIDKGLYCIIHHKKPTGM 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 167 ---NMLEYKGA-FSMEV---NVDYNASSETLRCEAPRWFPOPTVWASQVDOGAN 217
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 121 IRLHONMSELVLANFSQPIVPIISNTENVYI-NLTCSSIHGYPEP----- 166
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 218 FSEVSTNFEFLNSENVTMKY-----VSVLNVNTI-----NNTYSCMIEN 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 167 ---KKMSVLLRTKNSIEXDGIIMOKSQDVTLEYVISLSVSPDVTSNMKTIFCILET 222
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 257 DIKATGDIKVTSEIKR--RSHLQILNS---KASLCVSEFFAISM 297
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 223 DKTRLSSPFSIELEDPQPPDHPWITAVLPVITICVWFCLILW 268
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 14

```

; Sequence 23, Application PC/TUS9502576
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/02576
; CLASSIFICATION:
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/205,697
; FILING DATE: 02-Mar-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragoras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPCPC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 329 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-02576-23

```

Query Match 9.4%; Score 147.5; DB 5; Length 329;
 Best Local Similarity 23.4%; Pred. No. 5.3e-07;
 Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;

```

QY 50 IALIGFGISGRHSITVTTVASAGNIGEDGILCTF--EPDIKLSDIVIOMLKEGVGLV 107
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 12 ILFVMAFLLSGAAPLKIQAY-----FNETADLPCOFANSQOSISLSELYVMQOENL-VL 65
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 108 HEFEKGEDELSEODEMFRGTAVFADQVIYGNASLRKLNQVLDAQYKCYITTSKGG- 166
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

```

Db 66 NEVYLKREKEDSVHSHKMGTSFSDS-----SWTLRLHNIQIDKGLYCIIHHKKPTGM 120
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 167 ---NMLEYKGA-FSMEV---NVDYNASSETLRCEAPRWFPOPTVWASQVDOGAN 217
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 121 IRLHONMSELVLANFSQPIVPIISNTENVYI-NLTCSSIHGYPEP----- 166
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 218 FSEVSTNFEFLNSENVTMKY-----VSVLNVNTI-----NNTYSCMIEN 256
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 167 ---KKMSVLLRTKNSIEXDGIIMOKSQDVTLEYVISLSVSPDVTSNMKTIFCILET 222
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 257 DIKATGDIKVTSEIKR--RSHLQILNS---KASLCVSEFFAISM 297
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 223 DKTRLSSPFSIELEDPQPPDHPWITAVLPVITICVWFCLILW 268
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```

RESULT 15

```

; Sequence 2, Application PC/TUS9410257A
; GENERAL INFORMATION:
; APPLICANT: IMMLOGIC PHARMACEUTICAL CORPORATION
; APPLICANT: BRIGITTE DEVAUX
; APPLICANT: JONATHAN B. ROTHBARD
; APPLICANT: DAWN SMILEX
; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: IMMLOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02145
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: ASCII text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A
; FILING DATE: 1 SEPTEMBER 1994
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824
; FILING DATE: 03-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 071.1 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 247 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-10257A-2

```

Query Match 9.1%; Score 144; DB 5; Length 247;
 Best Local Similarity 20.8%; Pred. No. 7.6e-07;
 Matches 49; Conservative 39; Mismatches 80; Indels 68; Gaps 6;

```

QY 28 MASLQILFWSIISIIIL-----AGAILIIGFGISGRHSITVTTVASAGNIGED 78
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 1 MASLSRSLPSLSCSLFLLLLLVSSYAGQFV-----IGRHPRLAL-----VGDE 48
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
QY 79 GILSTFEPDIKLSDIVIOMLKEGVGLVHEFEKGEDELSEODEMFRGTAVFADQVIY 138
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |

```


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GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2002, 14:18:55 ; Search time 23.56 Seconds
(without alignments)
971.505 Million cell updates/sec

Title: US-09-636-801-392
Perfect score: 1574
Sequence: 1 HASAHASGRQRLHSASTQI.....SSFAISMAILPLSPYLMK 309

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 522463 seqs, 74073290 residues
Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : A_Geneseq_1101.*
1: /SIDSR/gcgdata/geneseq/AA1980.DAT.*
2: /SIDSR/gcgdata/geneseq/AA1981.DAT.*
3: /SIDSR/gcgdata/geneseq/AA1982.DAT.*
4: /SIDSR/gcgdata/geneseq/AA1983.DAT.*
5: /SIDSR/gcgdata/geneseq/AA1984.DAT.*
6: /SIDSR/gcgdata/geneseq/AA1985.DAT.*
7: /SIDSR/gcgdata/geneseq/AA1986.DAT.*
8: /SIDSR/gcgdata/geneseq/AA1987.DAT.*
9: /SIDSR/gcgdata/geneseq/AA1988.DAT.*
10: /SIDSR/gcgdata/geneseq/AA1989.DAT.*
11: /SIDSR/gcgdata/geneseq/AA1990.DAT.*
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21: /SIDSR/gcgdata/geneseq/AA2000.DAT.*
22: /SIDSR/gcgdata/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1574	100.0	309	21	AA12556
2	1574	100.0	309	22	AA12556
3	1431	90.9	282	21	AA12557
4	1431	90.9	282	21	AA12557
5	1431	90.9	282	22	AA12557
6	1431	90.9	282	22	AA12557
7	1431	90.9	282	22	AA12557
8	842.5	53.5	195	22	AA12557
9	301	19.1	63	22	AA12557
10	246	15.6	387	22	AA12557
11	246	15.6	441	22	AA12557

12	246	15.6	534	22	AA12556	Human B lymphocyte
13	246	15.6	534	22	AA12556	Human membrane or
14	246	15.6	534	22	AA12556	Human amyloid prec
15	246	15.6	1020	22	AA12556	Human polypeptide
16	245	15.6	340	22	AA12556	Human B lymphocyte
17	241	15.3	316	20	AA12556	Human PRO352 prote
18	241	15.3	316	21	AA12556	Human PRO352 (UNO3
19	239	15.2	244	22	AA12556	Human B7-H3 polype
20	239	15.2	316	22	AA12556	Human B7-H3 polype
21	239	15.2	316	22	AA12556	Human gene 2 encod
22	239	15.2	534	22	AA12556	Human amyloid prec
23	237	15.1	216	22	AA12556	Human polypeptide
24	232.5	14.8	216	22	AA12556	Human B7-H3 polype
25	232.5	14.8	216	22	AA12556	Human gene 2 encod
26	225.5	14.3	466	21	AA12556	Human PRO1472 (UNO
27	225.5	14.3	466	21	AA12556	Human membrane ass
28	225.5	14.3	466	22	AA12556	Human PRO1472. Ho
29	225.5	14.3	466	22	AA12556	Protein of the inv
30	225	14.3	327	22	AA12556	Gene #1 associated
31	225	14.3	349	22	AA12556	Secreted protein e
32	225	14.3	414	22	AA12556	Protein encoded by
33	224.5	14.3	461	21	AA12556	Bovine butyrophill
34	223	14.2	513	19	AA12556	Human secreted pro
35	222.5	14.1	461	21	AA12556	Human PRO1347 (UNO
36	222.5	14.1	500	21	AA12556	Human PRO1347. Ho
37	222.5	14.1	500	22	AA12556	Protein of the inv
38	222.5	14.1	500	22	AA12556	Gene 47 related pe
39	219.5	13.9	526	22	AA12556	Bovine butyrophill
40	219.5	13.9	526	20	AA12556	BBIR II protein en
41	218	13.9	319	21	AA12556	Bovine butyrophill
42	213.5	13.6	584	19	AA12556	Human butyrophill
43	211.5	13.4	526	20	AA12556	Human myelin oligo
44	209	13.3	223	19	AA12556	Human butyrophill
45	207.5	13.2	319	19	AA12556	Bovine butyrophill

ALIGNMENTS

RESULT 1	AA12556	standard; Protein: 309 AA.
ID	AA12556	
AC	AA12556	
XX	07-NOV-2000	(first entry)
XX	07-NOV-2000	
XX	Human: ovarian carcinoma antigen OBE protein SEQ ID NO:392.	
XX	Human: ovarian carcinoma; ovarian cancer; therapy; diagnosis;	
XX	tumour antigen; identification; cytostatic; gene therapy; vaccine.	
XX	Homo sapiens.	
XX	WO200036107-A2.	
XX	22-JUN-2000.	
XX	17-DEC-1999;	99NO-US30270.
XX	17-DEC-1998;	98US-0215681.
XX	17-DEC-1998;	98US-0216003.
XX	23-JUN-1999;	99US-0338933.
XX	24-SEP-1999;	99US-0404879.
XX	(CORI-) CORIXA CORP.	
XX	Mitcham JL, King GE, Algate PA, Frudakis TN;	
XX	WPI: 2000-431589/37.	
XX	Immunogenic portion of an ovarian carcinoma protein and the nucleic	
XX	acid encoding it, useful for the diagnosis, prevention and treatment of	

PT cancer, preferably ovarian cancer -
 XX
 PS Example 2; Page 205-206; 299pp; English.
 XX
 CC The present invention describes an isolated polypeptide comprising an
 CC immunogenic portion of an ovarian carcinoma protein (or its variants).
 CC Ovarian carcinoma proteins, and polynucleotides encoding them, have
 CC cytostatic activity and can be used in gene therapy and vaccines.
 CC Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines
 CC are useful for the prevention, diagnosis and treatment of cancer.
 CC preferably ovarian cancer. AA69691 to AA70077 and AAB12552 to AAB12557
 CC represent human ovarian carcinoma polynucleotides and proteins used in
 CC the exemplification of the present invention.
 CC
 XX
 SQ Sequence 309 AA:
 Query Match 100.0%; Score 1574; DB 21; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.4e-131;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASLGQILFWSTISITIIILAGATAIITGFGISG 60
 DB 1 hasahasgrqrlhsastqlrweppamaslqgllfwsilslililagatalilgfgisg 60
 QY RHSITVTVASAGNIGEDGILSTCFEPDRLSDIVIQWLKEGYLGVHEFEKGDSEI 120
 DB 61 rhsitvtvasagnigedgillstcfepdrlksdlvqlwkegylgvhefkegkdelseq 120
 QY 121 DEMFRGRTAVFAOVIVGNASRLKKNVQLTDACTYCYITTSKGNANLEYTGAFSMP 180
 DB 121 demfrgtravfadovivgnasrlknvqltdactykcyltskgnanleytgafsm 180
 QY 181 EVNVVDYNASSETLRCEAPRFPPQPTVYMASQVQGANFSEVSTSELSENVTKMVSV 240
 DB 181 evnvvdynassetlrceaprfppqptlvymasqvqganfsevsntsfelnsenvtkmvsv 240
 QY 241 LYNVTTNNYSCMIENDIAKATGDIKYTESEIKRRSHLQLNKASLVCSSFFAISMALL 300
 DB 241 lylvttntnyscmiendiakatgdikeyteiseikrrshlqlnksaslcvssffaismall 300
 -QY 301 PLSPYLMK 309
 DB 301 plspylmk 309
 RESULT 2
 AAB9205
 ID AAB9205 standard; Protein: 309 AA.
 XX
 AC AAB9205;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human ovarian tumour-derived antigen OBE #2.
 XX
 KW Cytostatic; human; breast tumour protein; breast cancer;
 KW ovarian tumour; antigen; OBE.
 XX
 OS Homo sapiens.
 XX
 PN WO200140269-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US32520.
 XX
 PR 30-NOV-1999; 99US-0451651.
 PR 22-FEB-2000; 2000US-0510662.
 PR 10-MAR-2000; 2000US-0523586.
 PR 07-APR-2000; 2000US-0545068.
 PR 15-MAY-2000; 2000US-0571025.
 XX

PA (CORI-) CORIXA CORP.
 PT
 XX Dillion DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
 XX WPI; 2001-356154/37.
 DR N-PDB; AAH55681.
 XX
 PT Breast tumor polypeptides and the nucleic acids that encode them,
 PT useful for the prevention, diagnosis and treatment of breast cancer -
 PS Example 3; Page 191-192; 221pp; English.
 CC
 CC The present invention relates to human breast tumour protein coding
 CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and
 CC AAH55682-AAH55762). The breast tumour protein DNA sequences may be used
 CC in the prevention, diagnosis and treatment of diseases associated with
 CC inappropriate expression of the breast tumour protein e.g. breast
 CC cancer. The present sequence is a human ovarian tumour-derived antigen,
 CC which was used in an example from the present invention.
 CC
 XX
 SQ Sequence 309 AA:
 Query Match 100.0%; Score 1574; DB 22; Length 309;
 Best Local Similarity 100.0%; Pred. No. 2.4e-131;
 Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HASAHASGRQRLHSASTQIRWEPSPAMASLGQILFWSTISITIIILAGATAIITGFGISG 60
 DB 1 hasahasgrqrlhsastqlrweppamaslqgllfwsilslililagatalilgfgisg 60
 QY RHSITVTVASAGNIGEDGILSTCFEPDRLSDIVIQWLKEGYLGVHEFEKGDSEI 120
 DB 61 rhsitvtvasagnigedgillstcfepdrlksdlvqlwkegylgvhefkegkdelseq 120
 QY 121 DEMFRGRTAVFAOVIVGNASRLKKNVQLTDACTYCYITTSKGNANLEYTGAFSMP 180
 DB 121 demfrgtravfadovivgnasrlknvqltdactykcyltskgnanleytgafsm 180
 QY 181 EVNVVDYNASSETLRCEAPRFPPQPTVYMASQVQGANFSEVSTSELSENVTKMVSV 240
 DB 181 evnvvdynassetlrceaprfppqptlvymasqvqganfsevsntsfelnsenvtkmvsv 240
 QY 241 LYNVTTNNYSCMIENDIAKATGDIKYTESEIKRRSHLQLNKASLVCSSFFAISMALL 300
 DB 241 lylvttntnyscmiendiakatgdikeyteiseikrrshlqlnksaslcvssffaismall 300
 -QY 301 PLSPYLMK 309
 DB 301 plspylmk 309
 RESULT 3
 AAB12557
 ID AAB12557 standard; Protein: 282 AA.
 XX
 AC AAB12557;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human ovarian carcinoma antigen OBE protein SEQ ID NO:393.
 XX
 KW Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
 KW tumour antigen; identification; cytostatic; gene therapy; vaccine.
 XX
 OS Homo sapiens.
 XX
 PN WO200036107-A2.
 XX
 PD 22-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US30270.
 XX

PR	17-DEC-1998;	98US-0215681.
PR	17-DEC-1998;	98US-0216003.
PR	23-JUN-1999;	99US-0338933.
PR	24-SEP-1999;	99US-0404879.
XX		
PA	(CORI-) CORIXA CORP.	
XX		
PI	Micham JL, King GE, Algate PA, Frudakis TN;	
XX		
DR	WPI: 2000-431589/37.	
PT	Immunogenic portion of an ovarian carcinoma protein and the nucleic acid encoding it, useful for the diagnosis, prevention and treatment of cancer, preferably ovarian cancer -	
XX		
PS	Example 2; Page 207; 299pp; English.	
CC	The present invention describes an isolated polypeptide comprising an immunogenic portion of an ovarian carcinoma protein (or its variants).	
CC	Ovarian carcinoma proteins, and polynucleotides encoding them, have	
CC	cytostatic activity and can be used in gene therapy and vaccines.	
CC	Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer,	
CC	preferably ovarian cancer. AAB69691 to AAB70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in the exemplification of the present invention.	
XX		
SO	Sequence 282 AA;	
Query Match	90.9%; Score 1431; DB 21; Length 282;	
Best Local Similarity	100.0%; Pred. No. 9.6e-119;	
Matches 282; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	28 MASLSQILFWSITISITIIAGATILITGSGISGRHSITVTVAASAGNIGEDGILSTPEP 87	
Db	1 maslsgqilfwsitisiilllagaiailligfsgsrnsilvtvtvasagngedgillstcep 60	
QY	88 DIKISDIIVIQWLKEGVGLVHEFKEGKDELSEODEFWGRTAVFADQVTVGNASLRLKNV 147	
Db	61 dklisdiivqlwkegvlglvhefkegkdelseqdemfrgtavfadqvivgnaslrlnkv 120	
QY	148 QLTDAQTKCYIITTSKGGKMANLEKTKGAFSMPEVNVVDYNASSETLRCEAPRMFPQPIYV 207	
Db	121 qltdagtkcyiitlskkgkmanleykkgafsmpevnavdy nassetlrceaprfwpqptvv 180	
QY	208 WASQVDGAGNSEVNTSEFELNSEWNTKVVSVLVLTNNTNNTNSCMTEINDIKATGDIYV 267	
Db	181 wasqvdgagansenvntsefelnsewntkvvsvlvltvlnntnyscmteindiatkgtldkv 240	
QY	268 TESIERSRSHQLNLNSKASLCVCSFFAISWALLPSPIYMLK 309	
Db	241 teselkrrshqnlnskascvcsffalswllpispymlk 282	
RESULT 4		
ID	AAY66719	
XX	AAY66719 standard; protein; 282 AA.	
XX		
AC	AAY66719;	
XX		
DT	05-APR-2000 (first entry)	
XX		
DE	Membrane-bound protein PRO1291.	
XX		
KW	Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor Immunoadhesin; gene mapping.	
XX		
OS	Homo sapiens.	
XX		
EN	W09963088-A2.	
XX		
DD	09-DEC-1999.	

XX	02-JUN-1999;	99WO-0812252.
PR	02-JUN-1998;	98US-0087607.
PR	02-JUN-1998;	98US-0087609.
PR	02-JUN-1998;	98US-0087759.
PR	03-JUN-1998;	98US-0087827.
PR	04-JUN-1998;	98US-0088021.
PR	04-JUN-1998;	98US-0088025.
PR	04-JUN-1998;	98US-0088028.
PR	04-JUN-1998;	98US-0088029.
PR	04-JUN-1998;	98US-0088030.
PR	04-JUN-1998;	98US-0088036.
PR	05-JUN-1998;	98US-0088167.
PR	05-JUN-1998;	98US-0088202.
PR	05-JUN-1998;	98US-0088212.
PR	05-JUN-1998;	98US-0088217.
PR	05-JUN-1998;	98US-0088655.
PR	10-JUN-1998;	98US-0088722.
PR	10-JUN-1998;	98US-0088730.
PR	10-JUN-1998;	98US-0088734.
PR	10-JUN-1998;	98US-0088738.
PR	10-JUN-1998;	98US-0088740.
PR	10-JUN-1998;	98US-0088742.
PR	10-JUN-1998;	98US-0088810.
PR	10-JUN-1998;	98US-0088811.
PR	10-JUN-1998;	98US-0088824.
PR	10-JUN-1998;	98US-0088825.
PR	10-JUN-1998;	98US-0088826.
PR	10-JUN-1998;	98US-0088858.
PR	11-JUN-1998;	98US-0088861.
PR	11-JUN-1998;	98US-0088863.
PR	11-JUN-1998;	98US-0088870.
PR	12-JUN-1998;	98US-0088906.
PR	12-JUN-1998;	98US-0089105.
PR	16-JUN-1998;	98US-0089440.
PR	16-JUN-1998;	98US-0089512.
PR	16-JUN-1998;	98US-0089514.
PR	17-JUN-1998;	98US-0089532.
PR	17-JUN-1998;	98US-0089598.
PR	17-JUN-1998;	98US-0089599.
PR	17-JUN-1998;	98US-0089600.
PR	17-JUN-1998;	98US-0089653.
PR	18-JUN-1998;	98US-0089801.
PR	18-JUN-1998;	98US-0089907.
PR	18-JUN-1998;	98US-0089908.
PR	19-JUN-1998;	98US-0089947.
PR	19-JUN-1998;	98US-0089948.
PR	19-JUN-1998;	98US-0089949.
PR	22-JUN-1998;	98US-0090245.
PR	22-JUN-1998;	98US-0090252.
PR	22-JUN-1998;	98US-0090254.
PR	23-JUN-1998;	98US-0090345.
PR	23-JUN-1998;	98US-0090346.
PR	24-JUN-1998;	98US-0090472.
PR	24-JUN-1998;	98US-0090535.
PR	24-JUN-1998;	98US-0090538.
PR	24-JUN-1998;	98US-0090540.
PR	24-JUN-1998;	98US-0090544.
PR	24-JUN-1998;	98US-0090445.
PR	25-JUN-1998;	98US-0090676.
PR	25-JUN-1998;	98US-0090678.
PR	25-JUN-1998;	98US-0090680.
PR	25-JUN-1998;	98US-0090691.

PR 25-JUN-1998; 98US-0090694.
 PR 25-JUN-1998; 98US-0090695.
 PR 25-JUN-1998; 98US-0090696.
 PR 26-JUN-1998; 98US-0090862.
 PR 26-JUN-1998; 98US-0090863.
 PR 01-JUL-1998; 98US-0091358.
 PR 01-JUL-1998; 98US-0091360.
 PR 01-JUL-1998; 98US-0091544.
 PR 02-JUL-1998; 98US-0091478.
 PR 02-JUL-1998; 98US-0091486.
 PR 02-JUL-1998; 98US-0091519.
 PR 02-JUL-1998; 98US-0091626.
 PR 02-JUL-1998; 98US-0091628.
 PR 02-JUL-1998; 98US-0091633.
 PR 02-JUL-1998; 98US-0091646.
 PR 02-JUL-1998; 98US-0091673.
 PR 07-JUL-1998; 98US-0091978.
 PR 07-JUL-1998; 98US-0091982.
 PR 09-JUL-1998; 98US-0092182.
 PR 10-JUL-1998; 98US-0092472.
 PR 20-JUL-1998; 98US-0093339.
 PR 30-JUL-1998; 98US-0094651.
 PR 04-AUG-1998; 98US-0095282.
 PR 04-AUG-1998; 98US-0095285.
 PR 04-AUG-1998; 98US-0095301.
 PR 04-AUG-1998; 98US-0095302.
 PR 04-AUG-1998; 98US-0095318.
 PR 04-AUG-1998; 98US-0095321.
 PR 04-AUG-1998; 98US-0095325.
 PR 10-AUG-1998; 98US-0095916.
 PR 10-AUG-1998; 98US-0095929.
 PR 10-AUG-1998; 98US-0096012.
 PR 11-AUG-1998; 98US-0096143.
 PR 11-AUG-1998; 98US-0096146.
 PR 12-AUG-1998; 98US-0096329.
 PR 17-AUG-1998; 98US-0096757.
 PR 17-AUG-1998; 98US-0096766.
 PR 17-AUG-1998; 98US-0096768.
 PR 17-AUG-1998; 98US-0096773.
 PR 17-AUG-1998; 98US-0096791.
 PR 17-AUG-1998; 98US-0096867.
 PR 17-AUG-1998; 98US-0096891.
 PR 17-AUG-1998; 98US-0096894.
 PR 17-AUG-1998; 98US-0096895.
 PR 17-AUG-1998; 98US-0096897.
 PR 18-AUG-1998; 98US-0096949.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096950.
 PR 18-AUG-1998; 98US-0096960.
 PR 18-AUG-1998; 98US-0097022.
 PR 19-AUG-1998; 98US-0097141.
 PR 20-AUG-1998; 98US-0097218.
 PR 24-AUG-1998; 98US-0097661.
 PR 26-AUG-1998; 98US-0097951.
 PR 26-AUG-1998; 98US-0097952.
 PR 26-AUG-1998; 98US-0097954.
 PR 26-AUG-1998; 98US-0097955.
 PR 26-AUG-1998; 98US-0097971.
 PR 26-AUG-1998; 98US-0097974.
 PR 26-AUG-1998; 98US-0097978.
 PR 26-AUG-1998; 98US-0097979.
 PR 26-AUG-1998; 98US-0097986.
 PR 26-AUG-1998; 98US-0098014.
 PR 31-AUG-1998; 98US-0098525.
 PR 16-SEP-1998; 98US-0100634.
 PR 12-JAN-1999; 99US-0115565.
 XX
 PA (GENETECH) GENENTECH INC.
 XX
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith Y, Watanabe CK;
 PI Wood WI, Yuan J;
 XX WPI: 2000-072883/06.
 DR

DR N-PSDB; AA265059.
 XX
 PT Membrane-bound proteins and related nucleotide sequences -
 XX
 PS claim 12; Fig 208; 822pp; English.
 XX
 CC The invention provides membrane-bound PRO polypeptides and
 CC polynucleotides encoding them. The PRO sequences of the invention were
 CC identified based on extracellular domain homology screening. The PRO
 CC sequences have homology with proteins including LDL receptors, TIE
 CC ligands and various enzymes. The membrane-bound proteins and receptor
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
 CC immunoadhesins, for instance, can be used as therapeutic agents to block
 CC receptor-ligand interactions. The membrane-bound proteins can also be
 CC employed for screening of potential peptide or small molecule inhibitors
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences
 CC are useful as hybridization probes. In chromosome and gene mapping and in
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences
 CC will also be useful for the preparation of PRO polypeptides, especially
 CC by recombinant techniques.
 XX
 SQ Sequence 282 AA:

Query Match 90.9%; Score 1431; DB 21; Length 282;
 Best local Similarity 100.0%; Pred. No. 9.6e-119;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 MASLGQILFWMSIISIIITAGATLITGICSRHSITVTYVNASAGNIGDGLSCTFPP 87
 Db 1 maslgqilfwmsiisiiitagaatalitgicrshtitvtvnsagngedgllscfep 60
 QY 88 DIRLSDIVTQWLEKGVLAGVHEFEKGRDELSEODEMFRGRTAVFAQVIVGNASRLKRV 147
 Db 61 dirlsdvltqwlkvgvlagvhefkegkdelseodemfrgrtavgadvivgnasrlkhnv 120
 QY 148 QLTDAITYKCYITTSKGRGNANLEFYTGAFPMEVVDVNASSETLRCAAPRFPOPTVY 207
 Db 121 qltdaitykcyilttskqgnanlefytgaftpmevvdvnassettlrceaprfpqlvv 180
 QY 208 MASOVDOGANFSEVNTSFELNSENVTKVSVLYVWTINNNTSCMIENDIKATGDIV 267
 Db 181 masovdoganfsevnstfelnsenvtkvsvlyvwtinnntyscmiendikaagdlkv 240
 QY 268 TESEIKRRSHLQLNKASLVCVSPFAISWALLPLSPYMLK 309
 Db 241 teselkrshlqlnksaslcvssffaiswallplspylmk 282

RESULT 5
 AAB99204
 ID AAB99204 standard; Protein; 282 AA.
 XX
 AC AAB99204;
 XX
 DT 04-SEP-2001 (first entry)
 XX
 DE Human ovarian tumour-derived antigen O8E #1.
 XX
 KW Cytostatic; human; breast tumour protein; breast cancer;
 KW ovarian tumour; antigen; O8E.
 OS Homo sapiens.
 XX
 PN WO200140269-A2.
 XX
 PD 07-JUN-2001.
 XX
 PF 29-NOV-2000; 2000WO-US32520.
 PF
 XX 30-NOV-1999; 99US-0451651.
 PR 22-FEB-2000; 2000US-0510662.
 PR 10-MAR-2000; 2000US-0523586.
 PR

```

PR 07-APR-2000; 2000US-0545068.
PR 15-MAY-2000; 2000US-0571025.
XX
PA (CORI-) CORIXA CORP.
XX
PI Dillon DC, Day CH, Jiang Y, Houghton RL, Mitcham JL, Wang A;
XX
DR WPI: 2001-356154/37.
XX N-PSDB; AAH55681.
XX
PT Breast tumor polypeptides and the nucleic acids that encode them,
XX useful for the prevention, diagnosis and treatment of breast cancer -
PS Example 3; Page 190; 221pp; English.
XX
CC The present invention relates to human breast tumour protein coding
CC sequences (see AAH55479-AAH55513, AAH55517-AAH55679 and
CC AAH55682-AAH55762). The breast tumour protein DNA sequences may be used
CC in the prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the breast tumour protein e.g. breast
CC cancer. The present sequence is a human ovarian tumour-derived antigen,
CC which was used in an example from the present invention.
XX
SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 22; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.6e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 MASLGGIILFMSIISIIIIILAGATALLIGFISGRHSITVTVTASAGNIGEDGILSCFEP 87
Db 1 maslggllflwsllslllllagaalalllgfsgshstltvtvasagnglgedgllscfep 60

OY 88 DIKLSDIVIOWLKEGVGLVHEFEKGDSEDEMRGRRTAVPADQVIVGNASLRKLV 147
Db 61 dklslsdlvlgwllkegvlglvhefkegkdelseqdemfgrgtavfadvivgnasllrkvv 120

OY 148 QLTDACTYKCYITTSKGGANLEKYGAFSMEPVNDVNASSETTLCEAPRPFPTVV 207
Db 121 qltdagtykcyiltstkgkgnanleyktgatsmpevndvnaasettlrcceaprfpqltv 180

OY 208 MASOVDOGANFSEVNTSFEINSENYTMKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
Db 181 wasqvogdganfsevnstsfelnseuvmkvsvlynvtnlncyscmiendiakatgdikv 240

OY 268 TESEIKRRSHLQNLNSKASLCVSSFFAISWALLPLSPYIMLK 309
Db 241 teseikrrshlqlnlskascvssffaiswallplspylimlk 282

RESULT 6
ID AAB87555 standard; Protein; 282 AA.
XX
AC AAB87555;
XX
DT 15-MAY-2001 (first entry)
XX
DE Human PRO1291.
XX
KW Human; PRO protein; mapping.
XX
OS Homo sapiens.
XX
PN WO200116318-A2.
XX
PD 08-MAR-2001.
XX
PF 24-AUG-2000; 2000WO-US23328.
XX
PR 01-SEP-1999; 99WO-US20111.
PR 15-SEP-1999; 99WO-US21090.

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PR 07-DEC-1999; 99US-0169495.
PR 09-DEC-1999; 99US-0170262.
PR 11-JAN-2000; 2000US-0175481.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 01-MAR-2000; 2000WO-US05601.
PR 03-MAR-2000; 2000US-0187202.
PR 25-APR-2000; 2000US-0199397.
PR 22-MAY-2000; 2000WO-US14042.
PR 05-JUN-2000; 2000US-0209832.
XX
PA (GETH ) GENENTECH INC.
XX
PI Eaton DL, Flyvareff E, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi CJ, Gurney AL, Matanabe CK, Wood WI;
XX
DR WPI: 2001-183260/18.
XX N-PSDB; AAF92087.
XX
PT Eighty four nucleic acids encoding PRO polypeptides, useful in
PT molecular biology, including use as hybridization probes, and in
PT chromosome and gene mapping.
XX
PS Claim 12; Fig 60; 278pp; English.
XX
CC The present sequence is a human PRO polypeptide (secreted and
CC transmembrane). The PRO protein, and PRO agonists, PRO antagonists or
CC anti-PRO antibodies are useful for preparation of a medicament useful in
CC the treatment of a condition which is responsive to the PRO protein,
CC agonists, antagonists or anti-PRO antibodies. The PRO protein may also be
CC employed as molecular weight markers for protein electrophoresis. The PRO
CC coding sequence has applications in molecular biology, including use as
CC hybridisation probes, and in chromosome and gene mapping.
XX
SQ Sequence 282 AA;

Query Match 90.9%; Score 1431; DB 22; Length 282;
Best Local Similarity 100.0%; Pred. No. 9.6e-119;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 MASLGGIILFMSIISIIIIILAGATALLIGFISGRHSITVTVTASAGNIGEDGILSCFEP 87
Db 1 maslggllflwsllslllllagaalalllgfsgshstltvtvasagnglgedgllscfep 60

OY 88 DIKLSDIVIOWLKEGVGLVHEFEKGDSEDEMRGRRTAVPADQVIVGNASLRKLV 147
Db 61 dklslsdlvlgwllkegvlglvhefkegkdelseqdemfgrgtavfadvivgnasllrkvv 120

OY 148 QLTDACTYKCYITTSKGGANLEKYGAFSMEPVNDVNASSETTLCEAPRPFPTVV 207
Db 121 qltdagtykcyiltstkgkgnanleyktgatsmpevndvnaasettlrcceaprfpqltv 180

OY 208 MASOVDOGANFSEVNTSFEINSENYTMKVSVLYNVTINNTYSCMIENDIAKATGDIKV 267
Db 181 wasqvogdganfsevnstsfelnseuvmkvsvlynvtnlncyscmiendiakatgdikv 240

OY 268 TESEIKRRSHLQNLNSKASLCVSSFFAISWALLPLSPYIMLK 309
Db 241 teseikrrshlqlnlskascvssffaiswallplspylimlk 282

RESULT 7
ID AAB65242 standard; Protein; 282 AA.
XX
AC AAB65242;
XX
DT 02-APR-2001 (first entry)
XX
DE Human PRO1291 (UN0659) protein sequence SEQ ID NO:291.

```

KW Human; secreted and transmembrane protein; PRO; cytosolic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.
 XX
 OS Homo sapiens.
 XX
 PN WO200073454-A1.
 XX
 PD 07-DEC-2000.
 XX
 PF 30-MAR-2000; 2000WO-US08439.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 23-JUN-1999; 99US-0141037.
 PR 07-JUL-1999; 99US-0143048.
 PR 20-JUL-1999; 99US-0144758.
 PR 26-JUL-1999; 99US-0145698.
 PR 28-JUL-1999; 99US-0146222.
 PR 17-AUG-1999; 99US-0149396.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 08-OCT-1999; 99US-0158663.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04341.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
 PI Ferrata N, Fong S, Gerbier H, Gerlitsen ME, Goddard A, Godowski PJ,
 PI Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT,
 PI Zhang Z;
 XX
 DR WPI: 2001-032160/04.
 DR N-PSDB; AAF44205.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 208; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytostatic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44470 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAF65154 to AAF65300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 282 AA;

Best Local Similarity 100.0%; Pred. No. 9.6e-119;
 Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 28 MASLQILEWISIIIIIIIIAGATLIIIGFCISGRHSITVTVTASAGNIGDGLSCFEP 87
 DB 1 maslqglllffwslslllllagaialllgfgisgrhsitvtvtasagngedgllscfep 60
 QY 88 DIKLSDIVIQWLKEGVGLVHEFEKGDDELSEODEMFRGTAVFAQOVYVGNASLRLKNV 147
 DB 61 dlksdlvlgwlkegylgvlvhefkegkdelsedemfrgtavfadqvlvgnaslrlknv 120
 QY 148 QLTDACTYKCYITTSKGNANLEKTAFAFSPFVVDVNASSETLRCEAPKPFQPTVY 207
 DB 121 qldactykyttskgynganlekytgaafspfvvdvnassettlrceaprfpqptvy 180
 QY 208 MASQVQGANFSEVNTSFELNSENVTMKVSVLYVWTINNTYSCMIENDIKATGDIVY 267
 DB 181 masqvqganfsevnstfelnsenvtmkvsvlyvwtlnntyscmlendikatktdivy 240
 QY 268 TSEIKRRSHLQILNSKASLCVSSFPFASWALLPLSPYMLK 309
 DB 241 tseikrrshlqlnksalcvssffafswallplspylmk 282
 RESULT 8
 AAB60776 standard; peptide: 195 AA.
 ID AAB60776
 AC AAB60776;
 DT 27-MAR-2001 (first entry)
 XX
 DE Gene 47 related peptide #2.
 XX
 KW Secreted protein; gene therapy; vaccine; cancer; leukemia;
 KW autoimmune disease; allergy; inflammation; graft rejection;
 KW hyperproliferation; cardiovascular; infection.
 XX
 OS Homo sapiens.
 XX
 PN WO200076531-A1.
 XX
 PD 21-DEC-2000.
 XX
 PF 01-JUN-2000; 2000WO-US15137.
 XX
 PR 11-JUN-1999; 99US-0138625.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Ruben SM, Komatsoulis GA;
 XX
 DR WPI: 2001-071148/08.
 XX
 PT Nucleic acids encoding 47 human secreted polypeptides, useful for
 PT preventing, diagnosing and/or treating e.g. cancers, Parkinson's
 PT disease and diabetic retinopathy -
 XX
 PS Disclosure; Page 524-525; 525pp; English.
 XX
 CC The present invention relates to 26 secreted human proteins. The
 CC proteins may be used in the prevention, diagnosis and treatment of
 CC diseases associated with inappropriate polypeptide expression.
 CC For example, they may be used in gene therapy or in vaccines.
 CC Typical of diseases which are potentially treatable are cancers
 CC (including leukemia), autoimmune diseases, allergies, inflammation,
 CC graft rejection, hyperproliferation, cardiovascular diseases
 CC (particularly critical limb ischemia and coronary disease) and any
 CC involving abnormal angiogenesis, neurodegeneration and/or
 CC infectious diseases.
 XX
 SQ Sequence 195 AA;

Query Match 90.9%; Score 1431; DB 22; Length 282;

Query Match 53.5%; Score 842.5; DB 22; Length 195;
 Best Local Similarity 82.1%; Pred. No. 7.4e-67;
 Matches 170; Conservative 3; Mismatches 9; Indels 25; Gaps 2;

QY 75 IGEGLISCFEPEDIKISDIYIOMLKRECVGLVHEFEKDELSQDEMRGFAVFEAD-133
 |||||
 Db 1 Igedgllstctfepdiklsdidiyglvhefkegq-----rxavgagx 48

QY 134 -----QYIVGNASRLKNNQLTDAGTYKCYITTSKGNANLEKTKGAFSME 181
 |||||

Db 49 nvqfpgqgclllkxxllmpilrllknvqltdaglykcylltskqgnanleyktgafsmpe 108
 |||||

QY 182 VNVVYNASSSETLRCEAPRMFPQPTVWVASQVDGANSFSEVNTSEFELSENVTMKVSVL 241
 |||||

Db 109 vnvynasssetlrceaprmfqpplvwvasqvdganfsevsntsfelnsenhvnmkvsvl 168
 |||||

QY 242 VNVNTINNTYSCMIENDIAKATGDIRVT 268
 |||||
 Db 169 ynvclnntyscmiendiakatgldikvt 195

RESULT 9
 AAM35874
 ID AAM35874 standard; Protein: 63 AA.

AC AAM35874;

DT 17-OCT-2001 (first entry)

DE Peptide #9911 encoded by probe for measuring placental gene expression.

KW Probe: microarray; human; placenta; antenatal diagnosis;

OS Homo sapiens.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

PT WPI; 2001-488897/53.

PS Human genome-derived single exon nucleic acid probes useful for

analyzing gene expression in human placenta -

Claim 27; SEQ ID NO 36143; 654pp; English.

Sequence 63 AA:

Query Match 19.1%; Score 301; DB 22; Length 63;

Best Local Similarity 92.1%; Pred. No. 1.4e-19;
 Matches 58; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 61 RHSTVTVVNASGNGEGGILSCFEPEDIKISDIYIOMLKRECVGLVHEFEKDELSQ 120
 |||||

Db 1 rhtstvtvtnasngngggilscfepediklsdidiyglvhefkegkdeelsq 60

QY 121 DEM 123
 |||

Db 61 dem 63

RESULT 10

AAB87415

ID AAB87415 standard; Protein: 387 AA.

AC AAB87415;

DT 22-MAY-2001 (first entry)

DE Human gene 2 encoded secreted protein fragment, SEQ ID NO:156.

KW Human; secreted protein; proliferative disorder; cancer; tumour;

KW foetal abnormality; developmental abnormality; haematopoietic disorder;

KW immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

KW inflammation; allergy; neurological disorder; Alzheimer's disease;

KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;

KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;

KW cardiovascular disorder; angiotensin disorder; kidney disorder;

KW gastrointestinal disorder; pregnancy-related disorder;

KW endocrine disorder; infection; wound healing; vunerarity;

KW cell culture; chemotaxis; food additive;

KW binding partner identification.

OS Homo sapiens.

PN WO200118022-A1.

PD 15-MAR-2001.

PF 31-AUG-2000; 2000WO-US24008.

PR 03-SEP-1999; 99US-0152315.

PR 03-SEP-1999; 99US-0152317.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ni J, Baker KP, Birse CE, Fiscella M, Komatsoulis GA, Rosen CA;

PI Soppet DR, Young PE, Ebner R, Duan DR, Olsen HS, Lafleur DM;

PI Moore PA, Shi Y, Wei Y, Florence KA;

DR WPI; 2001-203081/20.

Nucleic acid molecules encoding human secreted proteins, used in

preventing, treating or ameliorating a disorder, e.g. Alzheimer's and

Parkinson's diseases and cancers -

Disclosure; Page 14; 607pp; English.

AAFG1858-AAFG1929 represent cDNAs corresponding to 52 human secreted

protein genes, and AAB87342-AAB87413 represent the proteins they encode.

AAB87414-AAB87454 represent human secreted protein fragments. The genes

and their corresponding secreted proteins are useful for preventing,

treating or ameliorating medical conditions, e.g., by protein or gene

therapy. Pathological conditions can be diagnosed by determining the

amount of the new protein in a sample or by determining the presence of

mutations in the new genes. Specific uses are described for each of the

52 genes, based on the tissues in which they are most highly expressed,

and include developing products for the diagnosis or treatment of

proliferative disorders, cancer, tumours, foetal and developmental

abnormalities, haematopoietic disorders, diseases of the immune system,

AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation,

allergies, neurological disorders (e.g., Alzheimer's disease,

DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2941.
XX
KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PE 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QH, Zhou P, Goodrich R, Drmanac RT;
XX
DR WPI: 2001-442253/47.
DR N-PSDB: AAI58952.
XX
PT Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX
PS Example 4; SEQ ID NO 2941; 10078bp; English.
XX
CC The invention relates to human nucleic acids (AAI5798-AAI61369) and
CC the encoded polypeptides (AAM386A2-AAM4213) with nootropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
SQ Sequence 1020 AA;

Query Match 15.6%; Score 246; DB 22; Length 1020;
Best Local Similarity 26.2%; Pred. No. 4.8e-13;
Matches 76; Conservative 55; Mismatches 111; Indels 48; Gaps 13;

OY 19 QIRWEPSPAMASLGOI-----LF--WSIIIIIIIGALALITGFGI---SGRHS 63
DB 567 evfwgdgggvpplgnvltsgmanegllfdvshlrvlganglyscvlnpvlqgdahss 626
OY 64 ITVTVVAS-----AGNIGEDGILCTF--EPDIKLSDIYOWLKEGVLCV 107
DB 627 vltlprptgavveqvpedpvvalvgtdatlrscfspepfsiaqlnliwqltdtkqlv 686

OY 108 HEFKRGKDELSPQDEMFGRTRAVFADQYIVGNASRLKNVOTDAGTYKCYLIISKGN 167
DB 687 hstlegird---qgsayanraltlfpdliaqnaslrllqrvvadegstlct-vslrtdfqs 741
OY 168 ANLEKRTGA-FSPPEVNVVDYN-----ASSETLRCEAPMPFPQTVVMAISOVDGAFSEV 221
DB 742 aavslqvaapykspsmtlepnkdlrpgdltvltcssyrgypeaevf--qdgqgvpplgn 799
OY 222 SNTSPELNSENVTKRVSVLYNVT--INNYSCEIENDIAK--ATGDIVT 268
DB 800 vltsgmanegllfdvshlrvlganglyscvlnpvlqgdahsgvlt 848

Search completed: February 15, 2002, 14:20:18
Job time: 83 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:19:00 ; Search time 96.49 Seconds

(Without alignments)
889.170 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 3148936 seqs, 277657034 residues

Total number of hits satisfying chosen parameters: 3148936

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	1574	100.0	309	US-09-404-879A-392
2	1574	100.0	309	US-09-617-747-392
3	1574	100.0	309	US-09-636-801-392
4	1574	100.0	309	US-09-667-857-392
5	1574	100.0	309	US-09-778-320-209
6	1574	100.0	309	US-09-827-271-392
7	1574	100.0	309	US-09-884-441-392
8	1574	100.0	309	US-09-907-969-392
9	1574	100.0	309	US-09-910-689-209

10	1431	90.9	282	1	PCT-US01-20917-14	Sequence 14, App1
11	1431	90.9	282	1	PCT-US01-41430-5	Sequence 5, App1
12	1431	90.9	282	18	US-09-404-879A-393	Sequence 393, App
13	1431	90.9	282	20	US-09-617-747-393	Sequence 393, App
14	1431	90.9	282	20	US-09-636-801-393	Sequence 393, App
15	1431	90.9	282	20	US-09-667-857-393	Sequence 393, App
16	1431	90.9	282	21	US-09-709-328-291	Sequence 291, App
17	1431	90.9	282	21	US-09-778-320-208	Sequence 208, App
18	1431	90.9	282	22	US-09-827-271-393	Sequence 393, App
19	1431	90.9	282	22	US-09-850-178-33	Sequence 33, App
20	1431	90.9	282	22	US-09-884-441-393	Sequence 393, App
21	1431	90.9	282	23	US-09-896-738-2	Sequence 2, App1
22	1431	90.9	282	23	US-09-907-969-393	Sequence 393, App
23	1431	90.9	282	23	US-09-910-689-208	Sequence 208, App
24	1431	90.9	282	23	US-09-929-769-8	Sequence 8, App1
25	1431	90.9	282	23	US-09-941-992-291	Sequence 291, App
26	1431	90.9	282	23	US-09-950-083-5199	Sequence 5199, App
27	1320	83.9	258	22	US-09-896-738-3	Sequence 3, App1
28	1295	82.3	255	1	PCT-US01-20917-28	Sequence 27, App1
29	1184	75.2	231	1	PCT-US01-20917-28	Sequence 28, App1
30	1163	73.9	227	1	PCT-US01-41430-19	Sequence 19, App1
31	857.5	54.5	204	24	US-60-207-216-519	Sequence 519, App
32	842.5	53.5	195	1	PCT-US00-15137-132	Sequence 132, App
33	665	42.2	152	24	US-60-195-053-2748	Sequence 2748, App
34	593	37.7	116	22	US-09-896-738-7	Sequence 7, App1
35	484	30.7	93	22	US-09-896-738-8	Sequence 8, App1
36	480	30.5	94	24	US-60-169-840-5128	Sequence 5128, App
37	480	30.5	94	24	US-60-169-868-3684	Sequence 3684, App
38	434	27.6	84	24	US-60-160-209-3392	Sequence 3392, App
39	434	27.6	84	24	US-60-160-209-2463	Sequence 2463, App
40	348	22.1	65	20	US-09-617-747-415	Sequence 415, App
41	348	22.1	65	20	US-09-636-801-415	Sequence 415, App
42	348	22.1	65	20	US-09-667-857-415	Sequence 415, App
43	348	22.1	65	22	US-09-827-271-415	Sequence 415, App
44	348	22.1	65	22	US-09-884-441-415	Sequence 415, App
45	348	22.1	65	23	US-09-907-969-415	Sequence 415, App

ALIGNMENTS

RESULT 1

US-09-404-879A-392

Sequence 392, Application US/09404879A

GENERAL INFORMATION:

APPLICANT: Mitcham, Jennifer L.

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER

FILE REFERENCE: 210121.462C2

CURRENT APPLICATION NUMBER: US/09/404,879A

CURRENT FILING DATE: 1999-09-24

NUMBER OF SEQ ID NOS: 393

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 392

LENGTH: 309

TYPE: PRT

ORGANISM: Homo sapiens

US-09-404-879A-392

Query Match	100.0%	Score 1574;	DB 18;	Length 309;
Best Local Similarity	100.0%	Pred. No. 3.3e-152;		
Matches 309;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	HASAHASGRQLHSASTQIRMPSPAMASGQILFNSIIIIIIAGAILITGFGISG	60
DB	1	HASAHASGRQLHSASTQIRMPSPAMASGQILFNSIIIIIIAGAILITGFGISG	60

QY	61	RHSITVTTVASAGNIGEDGILSCFEPDIKLSDIVIQWLKGVGLVHFEKGDSEQ	120
DB	61	RHSITVTTVASAGNIGEDGILSCFEPDIKLSDIVIQWLKGVGLVHFEKGDSEQ	120

NUMBER OF SEQ ID NOS: 455
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-667-857-392

Query Match 100.0%; Score 1574; DB 20; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
DB 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
QY 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
DB 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
DB 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 5

US-09-778-320-209
Sequence 209, Application US/09778320
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yuguo
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Tongtong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C5
CURRENT APPLICATION NUMBER: US/09/778.320
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 301
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-778-320-209

Query Match 100.0%; Score 1574; DB 21; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
DB 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
QY 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120

DB 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
DB 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
DB 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 6

US-09-827-271-392
Sequence 392, Application US/09827271
GENERAL INFORMATION:
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary R.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C6
CURRENT APPLICATION NUMBER: US/09/827.271
CURRENT FILING DATE: 2001-04-04
NUMBER OF SEQ ID NOS: 461
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-271-392

Query Match 100.0%; Score 1574; DB 22; Length 309;
Best Local Similarity 100.0%; Pred. No. 5.3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
DB 1 HASAHASGRORQLHSASQIRWEPSPAMASLGQILFWSITIIITLGAIALIIGFGISG 60
QY 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCFTEPDIKLSDIYIQLKRGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
DB 121 DEMFRGRTAVFADQYIVGNASLRKKNVQITDAGTYKCYIITSKGGANLLEYKTGAFSMP 180
QY 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
DB 181 EVNVDYNASSSETLRCEARWFPQPTVYVASQVDOGANSEVNTSEFELNSEVNTKVVSV 240
QY 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
DB 241 LYNTVINTYSCMIENDIAKATGDIKVTSEIKRRSHQLNLSKASLCVSSFFAISMAL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 7

US-09-884-441-392
Sequence 392, Application US/09884441
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.

APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.462C7
CURRENT APPLICATION NUMBER: US/09/884,441
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-441-392

Query Match 100.0%; Score 1574; DB 22; Length 309;
Best Local Similarity 100.0%; Pred. No. 5,3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
DB 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
QY 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240
DB 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240
QY 241 LYVNTINNTYSCMIENDIAKATGDIVTESEIKRSHLQLLNSKASLCVSSFFAISWALL 300
DB 241 LYVNTINNTYSCMIENDIAKATGDIVTESEIKRSHLQLLNSKASLCVSSFFAISWALL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 8

US-09-907-969-392
Sequence 392, Application US/09907969
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon E.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Panger, Gary Richard
APPLICANT: Reed, Steven G.
APPLICANT: Veddyck, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.462C8
CURRENT APPLICATION NUMBER: US/09/907,969
CURRENT FILING DATE: 2001-07-17
NUMBER OF SEQ ID NOS: 596
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 392
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-907-969-392

Query Match 100.0%; Score 1574; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 5,3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
DB 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
QY 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240
DB 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240
QY 241 LYVNTINNTYSCMIENDIAKATGDIVTESEIKRSHLQLLNSKASLCVSSFFAISWALL 300
DB 241 LYVNTINNTYSCMIENDIAKATGDIVTESEIKRSHLQLLNSKASLCVSSFFAISWALL 300
QY 301 PLSPLYMLK 309
DB 301 PLSPLYMLK 309

RESULT 9

US-09-910-689-209
Sequence 209, Application US/09910689
GENERAL INFORMATION:
APPLICANT: Dillon, Davin C.
APPLICANT: Day, Craig H.
APPLICANT: Jiang, Yugu
APPLICANT: Houghton, Raymond L.
APPLICANT: Mitcham, Jennifer
APPLICANT: Wang, Jionglong
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.491C6
CURRENT APPLICATION NUMBER: US/09/910,689
CURRENT FILING DATE: 2001-07-20
NUMBER OF SEQ ID NOS: 307
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 209
LENGTH: 309
TYPE: PRT
ORGANISM: Homo sapiens
US-09-910-689-209

Query Match 100.0%; Score 1574; DB 23; Length 309;
Best Local Similarity 100.0%; Pred. No. 5,3e-152;
Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
DB 1 HASAHASGRQLHSASTOIRMEPPSPAMASLGQILFWSITITITILAGATALLIGFISG 60
QY 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
DB 61 RHSITVTVASAGNIGEDGILSCTFEPPDKLSDIVIOMLKEGVGLVHEFEKGDLSQ 120
QY 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
DB 121 DEMFRGRTAVFADQVIVGNASLRKNVQLTDAGTYKCYITTSKGNANLEYTKGAFSMP 180
QY 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240
DB 181 EVVNDYNASSETLRCEAPRFPOPTYVMAQVQGANFSEVNTSEFENSENTMKVSV 240

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; Db 181 EVAVDYNASSETLRCEAPRMPQPTVYVWASQVDOGANFSEVNTSEFELNSENVTMKVSV 240
;
; QY 241 LVAVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLOLNKASLCVSSFFAISWALL 300
;
; Db 241 LVAVTINNNTYSCMIENDIAKATGDIKVTSEIKRRSHLOLNKASLCVSSFFAISWALL 300
;
; QY 301 PLSPLYMLK 309
;
; Db 301 PLSPLYMLK 309
;
; RESULT 10
; PCT-US01-20917-14
; Sequence 14, Application PC/TUS0120917
;
; GENERAL INFORMATION:
; APPLICANT: Human Genome Sciences, Inc.
; TITLE OF INVENTION: B7-Like Polynucleotides, Polypeptides, and Antibodies
; FILE REFERENCE: PT124PCT
; CURRENT APPLICATION NUMBER: PCT/US01/20917
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-20917-14

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Query Match 90.9%; Score 1431; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; QY 28 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 87
;
; Db 1 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 120
;
; QY 148 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 309
;
; Db 241 TESEIKRRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 282
;
; RESULT 11
; PCT-US01-41430-5
; Sequence 5, Application PC/TUS0141430
;
; GENERAL INFORMATION:
; APPLICANT: Mayo Foundation for Medical Education and Research
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219M01
; CURRENT APPLICATION NUMBER: PCT/US01/41430
; CURRENT FILING DATE: 2001-07-26
; PRIOR APPLICATION NUMBER: 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5

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; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US01-41430-5

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Query Match 90.9%; Score 1431; DB 1; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; QY 28 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 87
;
; Db 1 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 120
;
; QY 148 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 309
;
; Db 241 TESEIKRRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 282
;
; RESULT 12
; US-09-404-879A-393
; Sequence 393, Application US/09404879A
;
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 393
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-404-879A-393

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Query Match 90.9%; Score 1431; DB 18; Length 282;
Best Local Similarity 100.0%; Pred. No. 2.1e-137;
Matches 282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; QY 28 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 87
;
; Db 1 MASLGOILFWSIIISIIILAGATALLIGFISGRHSITVTTVASAGNIGEDGILSCFEP 60
;
; QY 88 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 147
;
; Db 61 DIKLSDIVIOMLKEGVGLVHERKEGKDELSEODEMRGRTAFADQVYIGNASLRLKNV 120
;
; QY 148 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 207
;
; Db 121 QLTDACTYKCYIITSKKGANLEKYTGAFSMEPVNDVYNASSETLRCEAPRMPQPTV 180
;
; QY 208 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 267
;
; Db 181 WASQVDOGANFSEVNTSEFELNSENVTMKVSVLYVNTINNNTYSCMIENDIAKATGDIK 240
;
; QY 268 TESEIKRRSHLOLNKASLCVSSFFAISWALLPLSPYMLK 309

```



```

Db      121  QLTDACTYKCYIITSKSGNANLEYKTGAFSMPENVNDYNASSETLRCEAPRWFQPTVY 180
QY      208  WASOVDOGANFSEVSNTSEFENSENTVMKYVSVLYNTTINTYSCMIENDIAKATGDIKY 267
Db      181  WASOVDOGANFSEVSNTSEFENSENTVMKYVSVLYNTTINTYSCMIENDIAKATGDIKY 240
QY      268  TSEETKRSHLOLLNSKASLCVSSFFAISWALLPLSPYLMK 309
Db      241  TSEETKRSHLOLLNSKASLCVSSFFAISWALLPLSPYLMK 282

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Search completed: February 15, 2002, 14:22:24
 Job time: 204 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 15, 2002, 14:19:50 ; Search time 24.44 Seconds

(without alignments)
1849.351 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASRQRLQHSASQI.....SSFAISNALLPLSPYLMK 309

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: SP:REMBL_17:*
2: sp-archaea:*
3: sp-bacteria:*
4: sp-fungi:*
5: sp-human:*
6: sp_invertebrate:*
7: sp_mhcc:*
8: sp_mammal:*
9: sp-organelle:*
10: sp-plant:*
11: sp-rodent:*
12: sp-virus:*
13: sp-vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1425	90.5	282	4	09H6B2 homo sapien
2	247	15.7	316	4	09BXR1 homo sapien
3	225	14.3	220	4	09NM06 homo sapien
4	223	14.3	414	4	09UM44 homo sapien
5	223	14.2	513	4	000481 homo sapien
6	223	14.2	513	4	09HCY1 homo sapien
7	222.5	14.1	347	4	09H730 homo sapien
8	220	14.0	280	13	073716 grus amerle
9	219.5	13.9	286	6	046535 bos laurus
10	215.5	13.7	304	6	09BE26 macaca fasc
11	215.5	13.7	731	4	P78409 homo sapien
12	213.5	13.6	584	4	000478 homo sapien
13	209.5	13.3	526	4	09H458 homo sapien
14	208.5	13.2	334	4	09NR44 homo sapien
15	207.5	13.2	319	4	000477 homo sapien
16	207.5	13.2	334	4	09B081 homo sapien
17	207.5	13.2	357	4	015338 homo sapien
18	207.5	13.2	359	4	P78410 homo sapien
19	207.5	13.2	546	4	075658 homo sapien

20	204	13.0	350	4	099420 homo sapien
21	199.5	12.7	290	11	09EP73 mus musculu
22	196	12.5	296	13	042404 gallus gall
23	195.5	12.4	275	11	09JK39 mus musculu
24	193	12.3	527	4	000475 homo sapien
25	192	12.2	329	6	09XSX6 felis silve
26	192	12.2	332	6	09GM27 felis silve
27	189	12.0	586	4	09HCY2 homo sapien
28	188.5	12.0	290	4	09NR07 homo sapien
29	186	11.8	529	4	P78408 homo sapien
30	183	11.6	523	4	000480 homo sapien
31	181	11.5	280	6	09TTF1 09TTF1 canis fami
32	178	11.3	452	11	070355 mus musculu
33	176	11.2	313	11	035531 035531 rattus norv
34	175.5	11.1	455	4	09UR0 09UR0 homo sapien
35	172	10.9	329	6	09TTF2 09TTF2 canis fami
36	171.5	10.9	272	11	070356 mus musculu
37	171.5	10.8	432	4	09Y2C7 09Y2C7 homo sapien
38	169.5	10.8	284	6	09GL33 09GL33 bos taurus
39	168.5	10.7	391	11	035441 035441 mus musculu
40	166	10.5	326	11	070358 mus musculu
41	163	10.4	305	7	098261 098261 homo sapien
42	160.5	10.2	325	6	002838 sus scrofa
43	153.5	9.8	325	11	070359 070359 mus musculu
44	152.5	9.7	143	4	09NU62 09NU62 homo sapien
45	151	9.6	339	13	073892 073892 gallus gall

ALIGNMENTS

RESULT 1	
Q9H6B2	PRELIMINARY; PRT; 282 AA.
ID Q9H6B2	
AC Q9H6B2	
DT 01-MAR-2001 (TREMBLrel, 16, Created)	
DT 01-MAR-2001 (TREMBLrel, 16, Last sequence update)	
DT 01-JUN-2001 (TREMBLrel, 17, Last annotation update)	
DE CDNA: FLJ22418 FIS, CLONE HRC08590.	
OS Homo sapiens (Human).	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.	
OX NCBI_TaxID=9606;	
RN [1]	
RP SEQUENCE FROM N.A.	
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,	
RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,	
RA Tanaka T., Nakamura Y., Isegaki T., Sugano S.,	
RT "NDDO human CDNA sequencing project."	
RU Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.	
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX	
CC DOMAIN.	
CC EMBL: AK026071; BAB15349.1; -	
DR InterPro: IPR003599; Ig.	
DR InterPro: IPR003600; Ig_Like.	
DR InterPro: IPR003006; Ig_MHC.	
DR Pfam: PF00047; Ig; 1.	
DR SMART: SM00409; IG; 1.	
DR SMART: SM00410; IG_Like; 1.	
SO SEQUENCE 282 AA; 30893 MW; 6F9066999A1E9DB4 CRC64;	
Query Match	90.5%; Score 1425; DB 4; Length 282;
Best Local Similarity	99.6%; Pred. No. 4,4e-110;
Matches 281; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY 28 MASIGQLFWSTIIIIIIIGALNLTIGFGISGRHSITVTVAAGNIGEDGILSCFEP 87	
DB 1 MASIGQLFWSTIIIIIIIGALNLTIGFGISGRHSITVTVAAGNIGEDGILSCFEP 60	
QY 88 DIKLSDIVIOWLKEGVGLVHEFEKGRDELSEDEMFGRPTAVADQVYGNASLRKNV 147	
DB 61 DIKLSDIVIOWLKEGVGLVHEFEKGRDELSEDEMFGRPTAVADQVYGNASLRKNV 120	

QY	148	QLAGAGYKCYIIITISKGGANLEIKYKGAISMEPVANDYNASSETLLNCEAPRMEPQPTVV	207
Db	121	QLTAGYTKCYIIITISKGGANLEIKYKGAISMEPVANDYNASSETLLNCEAPRMEPQPTVV	180
QY	208	WASOVDCGANSEVSNTSFELNSENVMYKVVSVLYNTINTNTYSCTMIENDIAKATGDIK	267
Db	181	WASOVDCGANSEVSNTSFELNSENVMYKVVSVLYNTINTNTYSCTMIENDIAKATGDIK	240
QY	268	TESEIKRRSHPLQLNLSKASLCVSSFFAISMALPLSPYLMK	309
Db	241	TESEIKRRSHPLQLNLSKASLCVSSFFAISMALPLSPYLMK	282

RESULT	2
09BXRL	
ID	09BXRL
AC	09BXRL
DT	01-JUN-2001 (Tremblrel. 17, Created)
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE	COSTIMULATORY MOLECULE.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	Pubmed=11224528;
RA	Chapoval A.I., Ni J., Lau J.S., Wilcox R.A., Eiles D.B., Liu D.,
RA	Dong H., Sica G.L., Zhu G., Yamada K., Chen L.,
RT	"B7-H3: A costimulatory molecule for T cell activation and IFN-gamma
RT	production.";
RL	Nat. Immun. 2:269-274(2001).
DR	EMBL: AF302102; AAK15438.1;
SO	SEQUENCE 316 AA; 33791 MW; PF97007191CCEP1 CRC64;

Query Match	15.7%	Score 247;	DB 4;	Length 316;
Best Local Similarity	28.5%	Pred. No. 1.6e-12;		
Matches 74;	Conservative 46;	Mismatches 106;	Indels 34;	Gaps 10;

[illegible]

RESULT	3
Q9NM06	
ID	Q9NM06
AC	Q9NM06;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, last sequence update)
DT	01-JUN-2001 (TrEMBLrel. 17, last annotation update)
DE	CGMA FLJ20685 FIS. CLONE KAI1A3109.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo.
 OX NCBI_TaxID=9606;
 RN {}
 RP SEQUENCE FROM N.A.
 RC TISSUE=ILEAL MUCOSA;
 RA Tanigami A., Fujiwara T., Ono T., Yamada K., Fujii Y., Ozaki K.,
 RA Hiraio M., Ohmori Y., Ota T., Suzuki Y., Ohayashi M., Nishi T.,
 RA Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
 CC DOMAIN.
 CC
 DR EMBL: AK00692; BA91323.1; -.
 DR InterPro: IPR003599; Ig_.
 DR InterPro: IPR003600; Ig_Like.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00409; Ig_1.
 DR SMART: SM00410; Ig_Like_1.
 SO SEQUENCE 220 AA; 24979 MW; 66967620E130B515 CRC64;

	Query Match	14.3%	Score 225;	DB 4;	Length 220;
	Best Local Similarity	31.1%	Pred NO.6.4e-11;		
	Matches	61; Conservative	32; Mismatches	84; Indels	22; Gaps
OY	73 GNIGEDGILSCFEEDIKSLDIVIOMLKEGVGLVHEFEGKDSEODEMERGRTAVEA	132			
Dd	: : : : :	:	:	:	:
Dd	41 GRLEDILLPSFFE--RGSEEVIVIMKKYQDSY-KVHSYKGSGDHLESQPDRANRSTLELY	96			
OY	133 DOVIYGNASLRKANQLDADAGTYKCIIITSCKKGANALETKGAASMPENVNDYNASSET	192			
Dd	:::: :::::::	:	:	:	:
Dd	97 NEIQGNASNLSFRRLSLLDEGIITYCVGTALOVITNKVVALKGFELTPMKYEKRKTNSP	156			
OY	193 LRCEAPRMFPOTPVVMASOVDQA---NFSEV-SNTSELNSENVTMKVSVLVNYT-I	246			
Dd	: : : : :	:	:	:	:
Dd	157 LICSVLSSYPRIITW--KMONTPISENMMETSGLSDSI NSP-----LNITGS	204			
OY	247 NNTYSCTMIENDIAKAT	262			
Dd	: : : : :	:	:	:	:
Dd	205 NSSYEECTENSLKQT	220			

RESULT	4			
09UM44				
ID	09UM44	PRELIMINARY:	PRT:	414 AA.
AC	Q9UM44;			
DT	01-MAY-2000 (TrEMBLrel. 13, Created)			
DT	01-MAY-2000 (TrEMBLrel. 13, Last sequence update)			
DT	01-JUN-2001 (TrEMBLrel. 17, Last annotation update)			
DE	HERV-H LTR ASSOCIATING PROTEIN 2.			
GN	HHLA2.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93375318; PubMed=10444326;			
RA	Mager D. L., Hunter D. G., Schertzer M., Freeman J. D.;			
RT	"Endogenous retroviruses provide the primary polyadenylation signal			
RL	for two new human genes (HHLA2 and HHLA3).";			
CC	Genomics 59:255-263(1999).			
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX			
CC	DOMAIN.			
DR	EMBL: AF126162; AAD48396.1; -.			
DR	InterPro: IPR003559; Ig.			
DR	InterPro: IPR003600; Ig_Like.			
DR	InterPro: IPR003006; Ig_MHC.			
DR	Pfam: PF00047; Ig: 2.			
DR	SMART: SM00409; Ig: 2.			
DR	SMART: SM00410; Ig_Like; 1.			
QO	SEQUENCE 414 AA; 46850 MW; D645363E1562F70E CRC64;			

Query Match	14.38;	Score 225;	DB 4;	Length 414;
Best Local Similarity	31.18;	Pred. No. 1.5e-10;		
Matches 61;	Conservative 32;	Mismatches 81;	Indels 22;	Gaps 7;

QY	73	GNIEDILISTCFEPDJKLSIDIVYOWMLKEGVLGVHFEKGGKDLSFODEMFGRGTAVFA	132
Dd	41	GRLEDDILLSSFE---RGSEVVIHMKYQDSY-KVHSYYGSDHLESQDPRIANKRSLFY	96
QY	133	DQVIVGNASRLKANVOLLTAGYKCIIITSGKGNANILEYKTGAFSAPREVNDYNASSET	192
Dd	97	NEIQNGNASLFFRRVSLLDEGIYCYGTAIQTNNKVYLKVGVELPPMKYEKRNTNSF	156
QY	193	LRCACPMWFPQPIYVMAISOVDQA----NFSEV-SMTSFEINSENVTMAYVSVLYNVT-I	248
Dd	157	LICSVLSVYPRPILT--KKDNTPISENNMBETGLDFSFSINSP-----LNITGS	204
QY	247	NNTYSGMINDIAKAT	262
Dd	205	NSTSECTIENSILKOT	220

RESULT	5		
000481			
ID	000481	PRELIMINARY;	PRT: 513 AA.
AC	000481;		
DT	01-JUL-1997 (TReMBLrel, 04, Created)		
DT	01-JUL-1997 (TReMBLrel, 04, Last sequence update)		
DT	01-JUN-2001 (TReMBLrel, 17, Last annotation update)		
DE	BTYRAPHILIN.		
GN	BTFS.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Ruddy D.A., Kronmal G.S., Lee V.K., Mintler G.A., Quintana L.,		
RA	Domíngolo R., Meyer N.C., Basava A., McClelland E., Fullan A.,		
RA	Mapa F.A., Moore T., Thomas W., Loeb D.B., Harmon C., Tsuchihashi Z.,		
RL	Wolff R.K., Schatzman R.C., Feder J.N.;		
CC	Submitted (FEB-1987) to the EMBL/Genbank/DBJ databases.		
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX		
CC	DOMAIN:		
DR	EMBL: U90552; AAB53430.1; -		
DR	InterPro: IPR001870; Gamma_catboxylase.		
DR	InterPro: IPR003559; Ig.		
DR	InterPro: IPR003006; Ig_MHC.		
DR	InterPro: IPR003877; SPR.		
DR	Pfam: PF00047; Ig_1.		
DR	Pfam: PF00622; SPRy; 1.		
DR	SMART: SM00409; IG; 1.		
DR	SMART: SM00449; SPRy; 1.		
QO	SEQUENCE 513 AA; 57762 MW; CD334D7727CD1F63 CRC64;		

[illegible]

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OY      235 MKVV--SVLYVVTNNNYSCHEINDIAKAGDIVTESIEIKRSHTLOLMSKLAVSS- 291  
          :   |   |   |   |   |   |   |   |   |   |   |   |  
Db       201 LYVAASVIMMGSSGEEVSCTI-----RSSLLGLEKTASTSIADP 240
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OY      292 FF--AISM--ALLPLPYLM 308  
          |   |   |   |   |   |   |  
Db       241 FFSAQRIWIALATLEVL 261
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RESULT	6
09HCY1	
ID	09HCY1
AC	09HCY1; PRELIMINARY; PRT; 513 AA.
DT	01-MAR-2001 (TREMBLrel. 16, Created)
DT	01-MAR-2001 (TREMBLrel. 16, last sequence update)
DT	01-JUN-2001 (TREMBLrel. 17, last annotation update)
DE	D45P21.3 (BUTYROPHILIN, SUBFAMILY 3, MEMBER A1).
GN	BTN3A1.
OS	Homo sapiens (human).
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Phillips S.
RL	Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
CC	-1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR	EMBL: AL021917; GAC03424.1; -.
DR	InterPro: IPR001870; Gamma_carboxylase.
DR	InterPro: IPR003599; Ig.
DR	InterPro: IPR003006; Ig_MHC.
DR	InterPro: IPR003877; SPRY.
DR	Pfam: PF00047; Ig_1.
DR	Pfam: PF00622; SPRY; 1.
DR	SMART: SM00409; Ig_1.
DR	SMART: SM00449; SPRY; 1.
QO	SEQUENCE 513 AA; 57677 MW; 8D834D70526D1E6F CRC64;

Query Match	14.28:	Score 223:	DB 4:	Length 513:
Best Local Similarity	26.44:	Pred. No. 3e-10:		
Matches 69:	Conservative 44:	Mismatches 108:	Indels 40:	Gaps 10:
QY	62	HSITVTVTASAGNI----	GEDGILSCFTEPPDIKLSIDVIOMLKEGVGLVHEFEGKDEL	117
DB	27	HSAGSVGLPGSGPILAMGEDADLPCHLFPTMSAETMELKVVSSLRQVVNVYADGKEVE	86	
QY	118	SEODEMFGGRVAVFADQIVYGNASIRLKNQOLTAGTKCYIITSKGGNANLEKTKGAF	177	
DB	87	DROSAPYVGRSTSLRDGTITGAKRAALRHNVASDSGKLYFQODGFYKALVELKVAL	146	
QY	178	SMPEYVND---YNASSETLRCEAPRMPQPTVYVNASQYDQAGNSEVNTSFEIENSEVT	234	
DB	147	G-SPLHDVQKYGKOGGJHLECRSTGWYRQPIQNSN--NKGEN--IPTVEAPVADGVG	200	
QY	235	MKVY--SYLVNVTINNTYSCEMIENDIAKATGDIKTESIRRRSHLQLLNKASLCVSS-	291	
DB	201	LYAAVASVIMRGSGEGVSCFI-----RSSLLGLEKXTASISADP	240	
QY	292	FF--AISW--ALLPLSPYML	308	
DB	241	FFRSQRIWIALAGTLPVLL	261	
RESULT	7			
Q9H730				
ID	Q9H730	PRELIMINARY:	PRT:	347 AA.
AC	Q9H730:			
DT	01-MAR-2001 (Tremblrel. 16, Created)			
DT	01-MAR-2001 (Tremblrel. 16, Last sequence update)			
DT	01-JUN-2001 (Tremblrel. 17, Last annotation update)			
DE	CDNA: FLJ21458 FIS, CLONE COL04713.			


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RESULT 10
09BE26 PRELIMINARY; PRT; 304 AA.
ID 09BE26;
AC 09BE26;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE HYPOHETICAL. 33.1 KDA. PROTEIN.
OC Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
ON NCBI_TaxID=9541;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=FRONTAL CORTEX;
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries." (Apr-2001) to the EMBL/GenBank/DBJ databases.
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB060220; BAB41154.1; -.
KW Hypothetical protein.
SQ SEQUENCE 304 AA; 33103 MW; 962F3123610AD8A8 CRC64;

Query Match 13.7%; Score 215.5; DB 6; Length 304;
Best Local Similarity 27.4%; Pred. No. 6.1e-10;
Matches 55; Conservative 38; Mismatches 97; Indels 11; Gaps 6;

OY 75 IGEGLSCFTEPDIKLSIDIVIOMLKGVGLVHEFEKDELSODEMFRGRTAVFADQ 134
Db 44 VGEDADLPCHLPFWSETHLWVSSSLROYVNVADGKEVEDROSAPIRGKRSILRDD 103
OY 135 VIVGNASRLKNAVLTDACTYITSKGNANLEYKTAFA-SMPEVNV-DYNASSET 192
Db 104 IAGKALRIHNVTASDSGKLYCFQDGFYEKALVELKVALGSLNHLVEKVGEDGIIH 163
OY 193 LRCAPWFPQPTVYVNASQVDOGANSESVTSFELNSENVTKMYV--SVLYNTINTNTY 250
Db 164 LECSTWSTWPPKQIOWNSNA--KGNIPAV--EAPVYVADGVLAVASVIMRGSGSESV 218
OY 251 SCMIENDI--AKATGDIKYTE 269
Db 219 SCIRNSVGLKTKASTISAD 239

RESULT 11
P78409 PRELIMINARY; PRT; 731 AA.
ID P78409;
AC P78409;
DT 01-MAY-1997 (TReMBLrel. 03, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BT3.3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RL MEDLINE=98044204; PubMed=9382921;
RA Tazai-Ahmini R., Henry J., Offer C., Bouissou-Bouchouata C.,
RA Mather I.H., Pontarotti P.;
RT "Cloning, localization, and structure of new members of the
RT butyrophilin gene family in the juxta-telomeric region of the major
RT histocompatibility complex."
CC Immunogenetics 47:55-63(1997).
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: U97502; AAC02656.1; -.

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DR EMBL: U97500; AAC02656.1; JOINED.
DR EMBL: U97501; AAC02656.1; JOINED.
DR EMBL: U90143; AAC02651.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00622; SPRY; 1.
DR SMART: SM00409; IG; 1.
DR SMART: SM00449; SPRY; 1.
SQ SEQUENCE 731 AA; 81393 MW; 2F0E0A32B73685F0 CRC64;

Query Match 13.7%; Score 215.5; DB 4; Length 731;
Best Local Similarity 25.0%; Pred. No. 2.1e-09;
Matches 62; Conservative 49; Mismatches 110; Indels 27; Gaps 9;

OY 46 LAGAIA-LIIGFISGRHSITVTVASA-----GNIGEDGILSCFEPDIKLS 92
Db 1 MASSLAFLILNFHVS-LFVOLLTPCSAQSFLVGPSPILAMVEDADLPCHLFTPSAE 59
OY 93 DIVIWLKEGVLGVHEFEKDELSODEMFRGRTAVFADQVTVGNASRLKNAVLTDA 152
Db 60 TMELRWVSSSLRQVNVYVADGKEVEYRQSAPIRGKRSILRDKITAGKALRIHNVTASDS 119
OY 153 GTYKCIITTSKGNANLEYKTAFA-SMPEVNV--INASSETLRCAAPWFPQPTVYVNA 209
Db 120 GKLYCYFOHGDYFEKAPVELKVALG--SDLHIEKGVDDGDIHLECRSTGYVPOQIIMS 178
OY 210 SQVDGANFSEVSTSFELNSENVTKMYV--SVLYNTINTNTYSCMIENDI--AKATGDI 265
Db 179 D--SKENIPAVEG--PVNVYGVGLAVPPVINTGTSGGVCITINSLGLEKTAISI 233
OY 266 KTESEIK 273
Db 234 SIADPFQ 241

RESULT 12
O00478 PRELIMINARY; PRT; 584 AA.
ID O00478;
AC O00478;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Ruddy D.A., Krommal G.S., Lee V.K., Mintler G.A., Quintana L.,
RA Domingo R., Meyer N.C., Basava A., McClelland E., Fullan A.,
RA Mapa F.A., Moore T., Thomas W., Doeb D.B., Harmon C., Tsuchihashi Z.,
RA Wolff R.K., Schatzman R.C., Feder J.N.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Phillips S.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX
CC DOMAIN.
EMBL: U90548; AAB53426.1; -.
DR EMBL: AL021917; GAA17273.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003877; SPRY.
DR Pfam: PF00047; Ig; 1.
DR Pfam: PF00622; SPRY; 1.

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DR SMART: SM00409; IG: 1.
DR SMART: SM00449; SPRY: 1.
SQ SEQUENCE 584 AA; 65001 MW; 2B279B9141E0327F CRC64;

Query Match 13 6%; Score 213.5; DB 4; Length 584;
Best Local Similarity 24.6%; Pred. No. 2.7e-09;
Matches 60; Conservative 50; Mismatches 107; Indels 27; Gaps 9;

QY 46 LAGAAI-LIIGFISGRHSITVTTVASA-----GNIGEDGILCTFEEDPKLS 92
DB 3 MASSIAFLNLNHYV-LFVQLLTPCSAQSVLCPSPILLAMGEDADLPCHLFPPTSAE 61

QY 93 DIYIOMLKEGVGLVHEFEKDELSQDEMFGRRTAVFADQYVGNASLRKNVQLTDA 152
DB 62 TMELRWSSSLRQVYVNYADGKEVEDRQSAFYRGRTSILDGITAGKAALRHNVTSASD 121

QY 153 GTKCYIITSKGNANLEKTAFAFMEPVNV-----YNASSETLRCAFPWPOPTVMA 209
DB 122 GKLYCFQDDGEYKALVELKVALG-SDLHIEKGYEDGIGHLECRSTGWYPOQIKWS 180

QY 210 SQVDGAFSEVNTSEFELSENVTMKV--SVLYNTVINTYSCMIENDI--AKAGDI 265
DB 181 D--TKENIRPV---EAPVYADGVGLYAAVYIMRSGSGGVSCITRNSLLGLEKTA 235

QY 266 KYTE 269
DB 236 STAD 239

RESULT 13
ID 09H458 PRELIMINARY; PRT; 526 AA.

AC 09H458; 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BK14H9.2 (BUTYROPHILIN, SUBFAMILY 1, MEMBER A1).
GN BTN1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

DX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.

RA Tracey A.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.

DR EMBL: AL121936; CAC16802.1; -.
DR InterPro: IPR001870; Gamma_carboxylase.
DR InterPro: IPR003599; Ig.

DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR InterPro: IPR003877; SPRY.

DR Pfam: PF00047; Ig.1.
DR Pfam: PF00622; SPRY.1.
DR SMART: SM00409; IG.1.
DR SMART: SM00406; IG.V.
DR SMART: SM00410; IG_Like.1.
DR SMART: SM00449; SPRY.1.

SQ SEQUENCE 526 AA; 58960 MW; 4585D5CE88A2ECA4 CRC64;

Query Match 13.3%; Score 209.5; DB 4; Length 526;
Best Local Similarity 26.6%; Pred. No. 4.1e-09;
Matches 49; Conservative 37; Mismatches 93; Indels 5; Gaps 4;

QY 75 IGEDGILCTFEEDIKLSDIVIOMLKEGVGLVHEFEKDELSQDEMFGRRTAVFADQ 134
DB 42 VGEDADLPCHLFPPTMSAEHLEKTKVSPAVLVHROGDEADQMPYRGRATLVODG 101

QY 135 VIVGNASLRKNVQLTDAGTYKCIITSKGNANLEKTAFAFMEPVNVYNASSE-T 192
DB 102 IAKGVALLRIKGVAVSDGETCTCFREDGSEELVHLKAAALGSDPHISQVQENGEC 161

QY 193 LRCEAPRWFPQPTVMAVQVDGAFSEVNTSEFELSENVTMKVSVLYNTVINTYSC 252
DB 162 LECTSVGMWPEPQVQW--RTSKGKFPSTSE-SNPDEGLFTVVAASVILRDSAKNVSC 218

QY 253 MIEN 256
DB 219 YTON 222

RESULT 14
ID 09NR44 PRELIMINARY; PRT; 334 AA.

AC 09NR44; 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)

DE BUTYROPHILIN, SUBFAMILY 3, MEMBER A2.
GN BTN3A2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

DX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Rhodes D.A., Stammers M., Malcherek G., Beck S., Trowsdale J.;
RT "Genomic structure of the btf (butyrophilin-like) gene cluster on human chromosome 6.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
DR EMBL: AF257505; AAF6140.1; -.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig.1.
DR SMART: SM00409; IG.1.

SQ SEQUENCE 334 AA; 36399 MW; 95CFE887DBDBAE4 CRC64;

Query Match 13.2%; Score 208.5; DB 4; Length 334;
Best Local Similarity 26.1%; Pred. No. 2.7e-09;
Matches 55; Conservative 31; Mismatches 94; Indels 31; Gaps 5;

QY 75 IGEDGILCTFEEDIKLSDIVIOMLKEGVGLVHEFEKDELSQDEMFGRRTAVFADQ 134
DB 44 VGEDADLPCHLFPPTMSAEHLEKTKVSSILROYVYVNYADGKEVEDRQSAFYRGRTSILR 103

QY 135 VIVGNASLRKNVQLTDAGTYKCIITSKGNANLEKTAFAFMEPVNV-DYNASSET 192
DB 104 ITAGKAALRIHNVYASDSGKYLCDGDFEYKALVELKVALGSLHVEVKGEDGIGH 163

QY 193 LRCEAPRWFPQPTVMAVQVDGAFSEVNTSEFELSENVTMKVSV 240
DB 164 LECTSTGWTPOQIDGNAGKNIPAVPVADGGLYEVA-----ASV 208

QY 241 LYNTVINTYSCMIENDI--AKATGDIKYTE 269
DB 209 IMKSGSGEGVSCITRNSLLGLEKTAISTAD 239

RESULT 15
ID 000477 PRELIMINARY; PRT; 319 AA.

AC 000477; 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE BUTYROPHILIN.
GN BTF4.
OS Homo sapiens (Human).

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Result No.	Score	Query Match	Length	DB	ID	Description
1	219.5	13.9	526	2	A37821	butyrophilin - bovin
2	191.5	13.4	526	2	S70587	butyrophilin precu
3	171.5	10.9	487	2	S65133	butyrophilin - mou
4	168.5	10.7	391	2	T09058	butyrophilin homo
5	163.5	10.4	289	2	I46690	CD80 precursor - r
6	151	9.6	339	2	T28138	Ig V-region-like E
7	150.5	9.6	340	2	T28137	Ig V-region-like E
8	150	9.5	247	2	A55717	myelin/oligodendro
9	147.5	9.4	329	1	A48754	B7-2 antigen - hum
10	147.5	9.4	330	2	I46691	CD86 precursor - r
11	147	9.3	218	2	B47612	myelin/oligodendro
12	146.5	9.3	372	2	C39371	Ig V-region-like E
13	146	9.3	388	2	A39371	Ig V-region-like E
14	144	9.1	247	2	S58394	myelin/oligodendro
15	143.5	9.1	309	2	I49522	gene B7-2 protein
16	140.5	8.9	246	2	A47712	myelin/oligodendro
17	135	8.6	761	1	IJHUNG	neural cell adhesi
18	134.5	8.5	503	3	JC5287	SHP substrate-1 pr
19	133	8.4	1091	1	IJCJNL	neural cell adhesi
20	132.5	8.4	853	1	IJBNNG	neural cell adhesi
21	130.5	8.3	725	1	IJMNNG	neural cell adhesi
22	130.5	8.3	1033	2	S19247	cell adhesion prot
23	130.5	8.3	1115	1	IJMNLC	neural cell adhesi
24	128.5	8.2	858	1	IJRNLC	neural cell adhesi
25	127	8.1	946	1	A47299	ror-related recept
26	126.5	8.0	765	2	C42632	cell adhesion mole
27	126.5	8.0	812	2	B42632	cell adhesion mole
28	126.5	8.0	932	2	A42632	cell adhesion mole
29	126.5	8.0	1068	1	IJXJNL	neural cell adhesi

neural adhesion protein
B-lymphocyte antigen
neural cell adhesion
hypothetical protein
hemicholin precursors
protein-tyrosine kinase
protein-tyrosine kinase
dual protein - modulator
B-lymphocyte antigen
contactin precursor
sodium channel beta
cell-restricted
amalgam protein
Ig V-region-like B
hypothetical protein
neural cell adhesion

A; Accession: S/0587

R.; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc

QY 206 VMASVDQGAFSEVSNTSFELSENVTMAYSVL-YNVTINNTYSCHIENDIAKATGD 264
:
: : : : : : : : : : : : : :
Db 172 LAW---MEDGEETNAV-NTTVDQDDTELYSVSSELDENVTNNHSIVCLIK-----YGE 221

OY 265 IKYTE---SEIKRSHLOLNSKASLCVSSFFAISALLPLML 308
 Db 222 LVSQIFPWSKROEPPIDLP-----FWIIVSGALVL 256

RESULT 6

T28138
 Ig V-region-like B-G antigen, isoform 2 - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T28138
 R:Milne, S.; Kaufman, J.; Beck, S.
 submitted to the EMBL Data Library, May 1998
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A:Reference number: 220475
 A:Accession: T28138
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-339 <MIL>
 A:Cross-references: EMBL:AL023516; PIDN:CAA18959.1
 A:Experimental source: clone CB12
 C:Genetics:
 A:Gene: B-G 2
 A:Map position: 16
 A:Introns: 34/1; 148/1; 183/1; 189/1; 196/1; 203/1; 210/1; 217/1; 224/1; 231/1; 239/1; 2

Query Match 9.6%; Score 151; DB 2; Length 339;
 Best Local Similarity 21.7%; Pred. No. 0.00034;

Matches 56; Conservative 46; Mismatches 90; Indels 66; Gaps 10;

OY 63 SITVTYASAGNIGEDGILCTFEP--DIKLSDIYQWLKRGVGLVHEFEKGDSEQ 120
 Db 42 SLRYTAI-----VGDVVLRCOLSPCKDAMSSD--IRWIGHRTSGFVHHYONGED--LEQ 92
 OY 121 DEMRGRTAVFADQYIVGNASLRKNVOLTAGTYKCIITISKGGANLEKYGAFSMP 180
 Db 93 MEETKGRTELRLKGLSDGNLDLRITAVSTSDSGYSCAVLDGDGADA----- 140
 OY 181 EVNVYNASSETLRCEAPRMFPQPTVW-----ASQVDG 215
 Db 141 --VVDLEVSDP-----FSQITHPKKVALAVITVLVGSFVITVFLYRKKAETTKOK 189
 OY 216 ANFEVSNTSELSN-----ENVTMKVSVLVNTINTNT--YSCMIENDIAKATGDI-KVT 268
 Db 190 GKDELEGMADKLTGLAELERDPAKLETTVENLERNTFERAKKLASELERRNQLDKLA 249
 OY 269 ESEIKRSHLOLNSKAS 286
 Db 250 SDLVQOTKRAVEKLSQWS 267

RESULT 7

T28137
 Ig V-region-like B-G antigen, isoform 1 - chicken
 C:Species: Gallus gallus (chicken)
 C>Date: 15-Oct-1999 #sequence-revision 15-Oct-1999 #text_change 20-Jun-2000
 C:Accession: T28137
 R:Milne, S.; Kaufman, J.; Beck, S.
 submitted to the EMBL Data Library, May 1998
 A:Description: DNA sequencing and analysis of the chicken major histocompatibility comp
 A:Reference number: 220475
 A:Accession: T28137
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-340 <MIL>
 A:Cross-references: EMBL:AL023516; PIDN:CAA18958.1
 A:Experimental source: clone CB12
 C:Genetics:
 A:Gene: B-G 2
 A:Map position: 16
 A:Introns: 34/1; 148/1; 183/1; 190/1; 197/1; 204/1; 211/1; 218/1; 225/1; 232/1; 240/1; 2

Query Match 9.6%; Score 150.5; DB 2; Length 340;
 Best Local Similarity 32.4%; Pred. No. 0.00037;
 Matches 35; Conservative 22; Mismatches 40; Indels 11; Gaps 4;

OY 63 SITVTYASAGNIGEDGILCTFEP--DIKLSDIYQWLKRGVGLVHEFEKGDSEQ 120
 Db 42 SLRYTAI-----VGDVVLRCOLSPCKDAMSSD--IRWIGHRTSGFVHHYONGED--LEQ 92
 OY 121 DEMRGRTAVFADQYIVGNASLRKNVOLTAGTYKCIITISKGGANLEKYGAFSMP 180
 Db 93 MEETKGRTELRLKGLSDGNLDLRITAVSTSDSGYSCAVLDGDGADA 140

RESULT 8

A55717
 myelin/oligodendrocyte glycoprotein precursor - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 23-Mar-1995 #sequence-revision 23-Mar-1995 #text_change 08-Oct-1999
 C:Accession: A55717; C47712
 R:Daubas, P.; Pham-Dinh, D.; Dautigny, A.
 Genomics 23, 36-41, 1994
 A:Title: Structure and polymorphism of the mouse myelin/oligodendrocyte glycoprotein
 A:Reference number: A55717; MUID:95130110
 A:Accession: A55717
 A:Molecule type: DNA
 A:Residues: 1-247 <DAU>
 A:Cross-references: GB:L29498
 R:Pham-Dinh, D.; Mattei, M.G.; Nussbaum, J.L.; Rousset, G.; Pontarotti, P.; Roedel
 Proc. Natl. Acad. Sci. U.S.A. 90, 7990-7994, 1993
 A:Title: Myelin/oligodendrocyte glycoprotein is a member of a subset of the immunog
 A:Reference number: A47712; MUID:93376728
 A:Accession: C47712
 A:Molecule type: mRNA
 A:Residues: 30-95, 'E', 97-247 <PHA>
 A:Cross-references: GB:L20942; NID:g393588; PIDN:AAA03180.1; PID:g393589
 C:Genetics:
 A:Gene: MOG
 A:Map position: 17
 A:Note: encoded within the MHC
 C:Function:
 A:Description: may be involved in lipid interaction; may be involved in cell-cell c
 C:Keywords: glycoprotein; myelin; transmembrane protein
 F:1-29/Domain: signal sequence #status predicted <SIG>
 F:30-247/Product: myelin/oligodendrocyte glycoprotein #status predicted <MAT>
 F:151-119/Domain: transmembrane #status predicted <TM>
 F:204-229/Domain: transmembrane #status predicted <TM>
 F:60/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 9.5%; Score 150; DB 2; Length 247;
 Best Local Similarity 23.8%; Pred. No. 0.00027;
 Matches 34; Conservative 33; Mismatches 66; Indels 10; Gaps 2;

OY 37 WS-----IISIIILAGALILIGFISGRHSITVTYASAGNIGEDGILCTFEPDIK 90
 Db 5 WFSWPSQCFSLFLLL-----LQSCSYAGQFRTIGREYIRALVGBEALPCRLSPGKN 60
 OY 91 LSDIYQWLKRGVGLVHEFEKGDSEQDEMGRRTAVFADQYIVGNASLRKNVOLT 150
 Db 61 ATGMEVGVYRSPFSRVYILYRNGKDDAQAPEYRGRTELKETISEGKYLRIQNRFS 120
 OY 151 DAGTYKCIITISKGGANLEK 173
 Db 121 DEGGTCFFRDHSYQEEAAMELK 143

RESULT 9

A48754
 B7-2 antigen - human
 N:Alternate names: B7.0 glycoprotein; CD86 antigen; CTLA-4 counter-receptor
 C:Species: Homo sapiens (hmn)
 C>Date: 10-Sep-1999 #sequence-revision 10-Sep-1999 #text_change 10-Sep-1999

A:Accession: I49522
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-309 <RES>
A:Cross-references: GB:I25606; NID:q432478; PIDN:AA79770.1; PID:q432479
C:Genetics:
A:Gene: B7-2
C:Superfamily: B7-2 antigen

Query Match 9.1%; Score 143.5; DB 2; Length 309;
Best Local Similarity 22.6%; Pred.No. 0.0011;
Matches 50; Conservative 53; Mismatches 83; Indels 35; Gaps 10;

QY 64 ITVTIVASAGNT-----GEDGILSCTF--EPDIKLSDIVIOWLKEGVGLVHFEKRGKD 115
DB 15 VIVLLISDAVSVEYTAQVFNSTAYLPCPFKAQNISLSLVFWQDOOKL-VLEYHYLGTE 73
QY 116 ELSEODEMFRGRTAVFADQVIYGNASLRKKNVOLTQAGTYKCYITTSKGNANLEYK-- 173
DB 74 KLDVNAKTLGRTSF--DR--NNWTLRLHNVOIKDMGSYDCPTOKRPPTGSITILLQOTLT 128
QY 174 ---TGAFSMPEYVNDYNASSET--LRCEAPRMFPQPTVVMASQVDOGANFSEVSNTSF 226
DB 129 ELSVIANFSEPEIKLAQNTGTGNSGINLTCTSKGHPKPKMYFLITNSTNEYGD---NM 184
QY 227 ELNSENVTAKVSVLYNVTI-----NNTYSCMIENDIAK 260
DB 185 QISQDNVT-ELFSISNLSLSFPDGVVHMTVVCVLETESMK 224

Search completed: February 15, 2002, 14:20:40
Job time: 105 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: February 15, 2002, 14:20:20 ; Search time 9.96 Seconds

(without alignments)
1137.493 Million cell updates/sec

Title: US-09-636-801-392

Perfect score: 1574

Sequence: 1 HASAHASGRQLHSASTQI.....SSFAISNALPLSPYLMK 309

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: Listing first 45 summaries

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	215.5	13.7	526	1 BUTY_BOVIN	P18892 Bos taurus
2	211.5	13.4	526	1 BUTY_HUMAN	Q13410 homo sapien
3	178.5	11.3	524	1 BUTY_MOUSE	O62556 mus musculu
4	163.5	10.4	299	1 CD80_RABIT	P42070 coryctolagus
5	152	9.7	245	1 MOG_RAT	O63345 rattus norv
6	150.5	9.6	246	1 MOG_MOUSE	O61885 mus musculu
7	147.5	9.4	302	1 ICOL_HUMAN	O75144 homo sapien
8	147.5	9.4	329	1 CD86_HUMAN	P42081 homo sapien
9	147.5	9.4	330	1 CD86_RABIT	P42071 coryctolagus
10	144	9.1	247	1 MOG_HUMAN	O16653 homo sapien
11	143.5	9.1	309	1 CD86_MOUSE	P42082 mus musculu
12	140.5	8.9	246	1 MOG_BOVIN	P58033 bos taurus
13	135	8.6	761	1 NCAL_HUMAN	P13592 homo sapien
14	135	8.6	848	1 NCAL_HUMAN	P13591 homo sapien
15	132.5	8.4	853	1 NCAL_BOVIN	P18366 bos taurus
16	131	8.3	1091	1 NCAL_CHICK	P13590 gallus gall
17	130.5	8.3	725	1 NCAL_MOUSE	P13594 mus musculu
18	130.5	8.3	1115	1 NCAL_MOUSE	P13595 mus musculu
19	128.5	8.2	858	1 NCAL_RAT	P13596 rattus norv
20	126.5	8.0	1088	1 NCAL_MOUSE	P16170 xenopus lae
21	125.5	8.0	298	1 NCAL_HUMAN	P57087 homo sapien
22	124	7.9	306	1 CD80_MOUSE	O00609 mus musculu
23	123	7.8	365	1 CXAR_MOUSE	P97792 mus musculu
24	121	7.7	1010	1 CXAR_CHICK	P14781 gallus gall
25	120	7.6	215	1 CXAR_RAT	P54900 rattus norv
26	120	7.6	288	1 CXAR_HUMAN	P13681 homo sapien
27	120	7.6	333	1 CXAR_MOUSE	P13364 drosophila
28	120	7.6	365	1 CXAR_HUMAN	P18310 homo sapien
29	119	7.6	323	1 CXAR_MOUSE	O18066 caenorhabdi
30	115.5	7.3	1092	1 NCAL_XENILA	P36333 xenopus lae
31	114.5	7.3	322	1 ICOL_MOUSE	O91h38 mus musculu
32	113.5	7.2	1336	1 VGR1_RAT	P33767 rattus norv
33	113.5	7.2	1461	1 NEOL_HUMAN	O92859 homo sapien

34	113	7.2	359	1 LACH_DROME	Q24372 drosophila
35	112.5	7.1	337	1 G55A_CHICK	O98892 gallus gall
36	112.5	7.1	1018	1 CONT_HUMAN	O12860 homo sapien
37	112.5	7.1	1020	1 CONT_MOUSE	P12960 mus musculu
38	110	7.0	1036	1 AXOL_CHICK	P28685 gallus gall
39	109.5	7.0	1377	1 NEOL_RAT	P97603 rattus norv
40	107.5	6.8	351	1 CD2_HUMAN	O67729 homo sapien
41	106.5	6.8	347	1 CD2_HORSE	P37998 equus caball
42	106.5	6.8	413	1 HEMO_MANSE	P13398 manduca sex
43	106.5	6.8	1338	1 VGR1_HUMAN	P17948 homo sapien
44	106.5	6.8	1447	1 DCC_MOUSE	P70211 mus musculu
45	106	6.7	837	1 NCW2_MOUSE	O35136 mus musculu

ALIGNMENTS

RESULT 1
ID BUTY_BOVIN STANDARD: PRT: 526 AA.
AC P18892: 018955: 018959:
BT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYOPHILIN PRECURSOR (BT).
BT BTLAL OR BTN.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_Taxid=9913;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 27-47.
RX MEDLINE=9035441; PubMed=2387867;
RA JACK L.J.W., Mather I.H.;
RT "Cloning and analysis of cDNA encoding bovine butyrophillin, an apical
RT glycoprotein expressed in mammary tissue and secreted in association
RT with the milk-fat globule membrane during lactation.";
RL J. Biol. Chem. 265:14481-14486(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=HOLSTEIN-FRIESIAN;
RA Davey H.W., Ogg S.L., Husaini Y., Snell R.G., Korobko I.V.,
RA Mather I.H., Wilkins R.J.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RA Seyfert H., Luethen F.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP CARBOHYDRATE-LINKAGE SITES.
RX MEDLINE=9529316; PubMed=7775382;
RA Sato T., Takio K., Kobata A., Greenwalt D.E., Furukawa K.;
RT "Site-specific glycosylation of bovine butyrophillin.";
RL J. Biochem. 117:147-157(1995).
CC -1- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE.
CC -1- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN MAMMARY TISSUE AND SECRETED IN
CC ASSOCIATION WITH THE MILK-FAT-GLOBULE MEMBRANE DURING LACTATION.
CC -1- SIMILARITY: BELONGS TO THE IMMUGLOBULIN SUPERFAMILY. CONTAINS 1
CC V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
CC -1- SIMILARITY: STRONG. TO THE C-TERMINAL OF RET FINGER PROTEIN (RFP).
CC
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CC -----
CC EMBL: M35551; AAB39766.1; -
CC DR EMBL: AF005497; AAB62889.1; -
CC DR EMBL: Z93323; CAB07533.1; -
CC PIR: A37821; A37821
CC DR InterPro: IPR003879; Butyroph. DUF.C.
CC DR InterPro: IPR001870; Gamma_Cardxylase.
CC DR InterPro: IPR003006; Ig_MHC.
CC DR InterPro: IPR003596; Ig_V.
CC DR InterPro: IPR003877; SPRY.
CC DR Pfam: PF00047; Ig_1.
CC DR Pfam: PF00622; SPRY; 1.
CC DR SMART: SM00406; Igv; 1.
CC DR SMART: SM00449; SPRY; 1.
CC KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
CC FT SIGNAL 1 26
CC FT CHAIN 27 526 BUTYROPHILIN,
CC FT DOMAIN 27 242 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 243 269 POTENTIAL.
CC FT DOMAIN 270 526 CYTOPLASMIC (POTENTIAL).
CC FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
CC FT CARBOHYD 215 215 N-LINKED (GLCNAC. . .) (HYBRID).
CC FT CONFLICT 35 35 Q -> P (IN REF. 3).
CC FT CONFLICT 220 230 E -> D (IN REF. 1).
CC SQ SEQUENCE 526 AA: 59276 MW; A14126802BD19284 CRC64;

Query Match 13.7%; Score 215.5; DB: 1; Length 526;
Best Local Similarity 24.5%; Pred. NO.3.4e-10;
Matches 48; Conservative 49; Mismatches 94; Indels 5; Gaps 4;

OY 75 ISEEDILSCTFEPDIKLSDIVIOWLKEGVGLVHEFEKGGKDELSEODEMFCRGRVAFADQ 134
DB 42 VEGDADELPCRLSPNVSASAKMELRMFRREKVPAYFVSRQEGDEGEEMAEKGRVSLVEDH 101
OY 135 VIVGNASLRLKNAVLTLDAGTYKCYITTSKGNANLEKYKGAFL-SMPEVNDYNASSE-T 192
DB 102 IAEGSVAVARIQEVKASDDEYRCFPRODENEEALIVHLKVALGSDPHISMKVGESEIQ 161
OY 193 LKCEAPRMPEPPOTVYVWASOVDOGAMFSEVSNSEFLSEENTYMKVSVLVYNTINTYSC 252
DB 162 LECTSGVGRPEQOVOM--RTIRGEEFPSSKESRNPDEEGELTVRASVITIRDSMKNV-SC 218
OY 253 MIENDIAKATGDIKYT 268
DB 219 CIRNLLLGQEKREVEVS 234

RESULT 2
BUTY_HUMAN
ID BUTY_HUMAN STANDARD: PRT: 526 AA.
AC Q13410:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BUTYROPHILIN PRECURSOR (BT).
GN BTN1A1 OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human butyrophilin reveals a
RT potential receptor function.";
RL Biochim. Biophys. Acta 1306:1-4(1996).
CC -!- FUNCTION= MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT

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[illegible]

FT DOMAIN 42 122 IG-LIKE V-TYPE DOMAIN.
 FT DOMAIN 154 222 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 49 115 POTENTIAL.
 FT DISULFID 161 215 POTENTIAL.
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 88 88 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 97 97 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 122 122 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 185 185 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 299 AA: 33513 MW: 67442235C91DE0 CRC64;

Query Match 10.4%; Score 163.5; DB 1; Length 299;
 Best Local Similarity 25.3%; Pred. No. 2.9e-06;
 Matches 73; Conservative 57; Mismatches 89; Indels 69; Gaps 19;

QY 40 ISIIILAGALIIIGFISGRHSITVTVAAGNIGEDGILSCPEPDI-KLSDIYIOW 98
 DB 19 LCLLLLAG---LHFSGSI---QVTK-----SYKEMALSCDYNISIDELARKHITV 65
 QY 99 LKGG--VLGLVHEKKEKDELSEODEMFRGRTAVFADQVTVGNASLRKNVQLTDAGTYK 156
 DB 66 QKDOQWLSIIT---SGQVEYVPE---YKNRT--FPD--LIINLSMILIALRLSDKGT 114
 QY 157 CYIITSKGNANLEKTKGA-----FSMPKV---NDYNASSEFLRCEAPRPFPOPT 205
 DB 115 C-VVQKNEKSGFRRLTSTVLSIRADFPVPSITDIGHPDNN--KRIRCSAGSGPEPR 171
 QY 206 VVWASOVDOGANFSEVNTSELSNENVTWKVYSVL-YNTINTNTSCMIENDIANATGD 264
 DB 172 LAM---MEDGELINAV-NITVDDDLTELYSVSELDENVTNHSHVCLIK-----YGE 221
 QY 265 IKVTE---SEIKRSHLQLLNSKASLCVSSFPFISWALLPLSPYML 308
 DB 222 LVSQIFPWSKPKQEPPIQLP-----FWIIPVSGALVL 256
 RESULT 5
 MCG_RAT STANDARD; PRT; 245 AA.
 ID MCG_RAT 063345;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
 GN MCG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=93085763; PubMed=1453482;
 RA Gardiner M.V., Amliquet P., Lington C., Mathieu J.-M.,
 "Myelin/oligodendrocyte glycoprotein is a unique member of the
 immunoglobulin superfamily."
 RT J. Neurosci. Res. 33:177-187(1992).
 RL [2]
 RP SEQUENCE OF 28-245 FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,
 Pontarotti P., Roeckel N., Mather I.H., Artzt K., Lindahl K.F.,
 Dautigny A.;
 "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
 immunoglobulin superfamily encoded within the major
 histocompatibility complex."
 RT Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RL [3]
 RP STRUCTURE BY NMR OF 62-82.
 RX MEDLINE=97354172; PubMed=9210466;

RA Albouze-Abo S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
 RT "A conformational study of the human and rat encephalitogenic myelin
 oligodendrocyte glycoprotein peptides 35-55."
 RL Eur. J. Biochem. 246:59-70(1997).
 CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
 CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
 CC CELL COMMUNICATION.
 CC -1- SUBUNIT: MAY FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
 CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
 CC MEMBRANES.
 CC -1- DEVELOPMENTAL STAGE: A PEAK OF EXPRESSION HAS BEEN OBSERVED
 CC BETWEEN POSTNATAL DAYS 15 AND 25, COINCIDENT WITH THE PERIOD OF
 CC ACTIVE MYELINATION.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE V-LIKE DOMAIN. BELONGS TO THE BTN/MOG SUBFAMILY.
 CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
 CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
 CC
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 CC
 DR EMBL: M99485; AAA41628.1; -
 DR EMBL: L21995; AAF74766.1; -
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; IgV.1.
 DR SMART: SM00406; IgV.1.
 KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 245 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
 FT DOMAIN 28 155 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 156 176 POTENTIAL.
 FT DOMAIN 177 208 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 209 229 POTENTIAL.
 FT DOMAIN 230 245 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 44 132 IG-LIKE V-TYPE DOMAIN.
 FT DISULFID 51 125 POTENTIAL.
 FT CARBOHYD 58 58 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 245 AA: 27881 MW: C97F8AD06D6A32B4 CRC64;

Query Match 9.7%; Score 152; DB 1; Length 245;
 Best Local Similarity 26.2%; Pred. No. 1.9e-05;
 Matches 39; Conservative 31; Mismatches 55; Indels 24; Gaps 5;

QY 37 WS-----IISIIIL-----AGAILIIGFISGRHSITVTVAAGNIGEDGILSC 84
 DB 5 WSLSLPSCLSLLLLQLSLRSTAGGR-VIGRG-----HPIRL-----VGDALLPCR 52
 QY 85 FEPDIKLSDIYIOWLKEGVGLVHEKKEKDELSEODEMFRGRTAVFADQVTVGNASLR 144
 DB 53 ISPGKNATGMEVGMVRSRNVHLRYNGDQADQAPVGRFTLLKESIGGKVALRI 112
 QY 145 KNYQLTDAGTYKCYITTSKGNANLEK 173
 DB 113 QNVFSDGGYTCFPRDHSYOEBAVELK 141
 RESULT 6
 MCG_MOUSE STANDARD; PRT; 246 AA.
 ID MCG_MOUSE 061885; Q62003; P70364;
 AC 061885; Q62003; P70364;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.

GN MOG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_TaxID=10090;
 RX (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129;
 RX MEDLINE=95130110; PubMed=7829100;
 RA Dabbs P., Pham-Dinh D., Dautigny A.;
 RT "Structure and polymorphism of the mouse myelin/oligodendrocyte
 RT glycoprotein gene.";
 RL Genomics 23:36-41(1994).
 RN (2)
 RP SEQUENCE FROM N.A.
 RA Gardiner M.V., Mathieu J.M.;
 RT "Murine and human MOG are highly conserved: cDNA analysis."
 RL Trans. Am. Soc. Neurochem. 24:234-234(1993).
 RN (3)
 RP SEQUENCE OF 29-246 FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Rousset G.,
 RA Pontarotti P., Roessel N., Mather I.H., Artzt K., Lindahl K.F.,
 RA Dautigny A.;
 RT "Myelin/oligodendrocyte glycoprotein is a member of the
 RT immunoglobulin superfamily encoded within the major
 RT histocompatibility complex.";
 RL Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RN (4)
 RP SEQUENCE OF 29-54.
 RC STRAIN=BALB/C; TISSUE=Brain;
 RX MEDLINE=92218912; PubMed=1373175;
 RA Amiguet P., Gardiner M.V., Zanetta J.-P., Mathieu J.-M.;
 RT "Purification and partial structural and functional characterization
 RT of mouse myelin/oligodendrocyte glycoprotein.";
 RL J. Neurochem. 58:1676-1682(1992).
 CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
 CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
 CC CELL COMMUNICATION.
 CC -1- SUBUNIT: MAY FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
 CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
 CC MEMBRANES.
 CC -1- DISEASE: REDUCED CONCENTRATIONS OF MOG ARE OBSERVED IN JIMPY AND
 CC QUACKING DYSMYELINATING MUTANT MICE.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE V-LIKE DOMAIN. BELONGS TO THE B2M/MOG SUBFAMILY.
 CC -1- CAUTION: DO NOT CONFUSE MYELIN OLIGODENDROCYTE GLYCOPROTEIN (MOG)
 CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: L29503; AAC42023.1; -;
 DR EMBL: L29498; AAC42023.1; JOINED.
 DR EMBL: L29500; AAC42023.1; JOINED.
 DR EMBL: L29501; AAC42023.1; JOINED.
 DR EMBL: L29499; AAC42023.1; JOINED.
 DR EMBL: L29502; AAC42023.1; JOINED.
 DR EMBL: U64572; AAB08096.1; -;
 DR EMBL: L20942; AAA03180.1; -;
 DR MGD: MGI:97435; MOG.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SMO0406; IgV_1.

KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 246
 FT DOMAIN 29 156 MYELIN OLIGODENDROCYTE GLYCOPROTEIN.
 FT TRANSMEM 157 177 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 178 209 POTENTIAL.
 FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 231 246 POTENTIAL.
 FT DOMAIN 45 133 EXTRACELLULAR (POTENTIAL).
 FT DISULFD 52 126 IG-LIKE V-TYPE DOMAIN.
 FT CARBOHYD 59 59 POTENTIAL.
 FT CONFLICT 21 21 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 32 32 L -> G (IN REF. 2).
 FT CONFLICT 95 95 R -> G (IN REF. 4).
 FT CONFLICT 169 169 G -> E (IN REF. 3).
 FT CONFLICT 169 169 P -> S (IN REF. 2).
 SO SEQUENCE 246 AA; 28271 MW; 1F1AB44A0D5CFB89 CRC64;
 Query Match 9.6%; Score 150.5; DB 1; Length 246;
 Best local similarity 23.8%; Pred. No. 2.5e-05;
 Matches 34; Conservative 33; Mismatches 65; Indels 11; Gaps 2;
 Oy 37 WS-----TSTIIITAGALILIGFISGRHSITVTVASAGNIGEDGILSCTEPPDK 90
 Db 5 WFSWSPSCFLSLILL-----LQLSCSYAGQPRVIGPGYPIRALVGDEALELPCRSIPKN 59
 Oy 91 LSDIYIOMKEVGLVHEFEKQDELSEODEMFGRVAFVDQYIVGNASRLKNQLT 150
 Db 60 AIGMEVGVWRSPSPRVVHLHYRNGKDQDAQAEYRGRELLKETSIGKVTLRIQNVRS 119
 Oy 151 DAGTKCYITTSKGNANLEK 173
 Db 120 DEGGTTCFPRDHSYGEANAEK 142
 RESULT 7
 ICOL_HUMAN STANDARD: PRT: 302 AA.
 ID 075144; Q9NR01; Q9HD18;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ICOS LIGAND PRECURSOR (B7 HOMOLOG 2) (B7-H2) (B7-LIKE PROTEIN GL50)
 DE (B7-RELATED PROTEIN-1) (B7RP-1).
 GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 ON NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Dendritic cell;
 RX PubMed=11023515;
 RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;
 RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds
 RT ICOS.";
 RL Blood 96:2808-2813(2000).
 RN (2)
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RC TISSUE=Peripheral blood lymphocytes;
 RX PubMed=11007762;
 RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,
 RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han K.,
 RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Cocchia M.A.;
 RT "Characterization of a new human B7-related protein: B7RP-1 is the
 RT ligand to the co-stimulatory protein ICOS.";
 RL Int. Immunol. 12:1439-1447(2000).
 RN (3)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=20126021; PubMed=10657606;
 RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
 RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,

RA Jacobs K.A., Collins M.;
 RT "Identification of GLS0, a novel B7-like protein that functionally
 RT binds to ICOS receptor.";
 RL J. Immunol. 164:1653-1657(2000).
 RN (4)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98403880; PubMed=9734811;
 RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,
 RA Kotani H., Nomura N., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. X.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro.";
 RL DNA Res. 5:169-176(1998).
 RN (5)
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RA Ling V., Dunussi-Joannopoulos K.;
 RT "G150 molecules and uses therefor.";
 RL Patent number WO0121796, 29-MAR-2001.
 CC -1- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: AT LEAST 2 ISOFORMS: 1 (SHOWN HERE) AND 2;
 CC ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,
 CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE
 CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUCOCYTES,
 CC SPLEEN, THYMUS AND TONSIL). WHILE ISOFORM 2 IS DETECTED ONLY IN
 CC LYMPH NODES, LEUCOCYTES AND SPLEEN.
 CC -1- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY
 CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND
 CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.
 CC -1- SIMILARITY: CONTAINS 1 C2-LIKE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 V-LIKE DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. B7N/MOG
 CC SUBFAMILY.
 CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN IN POSITION 300
 CC ONWARD FOR AN UNKNOWN REASON.
 CC CC
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 CC
 CC EMBL: AF199028; AAF34739.1; -;
 CC EMBL: AF289028; AAG01176.1; -;
 CC EMBL: AF216749; AAK16241.1; -;
 CC EMBL: AB014553; BAA31628.1; ALT_SEQ.
 CC EMBL: AX100595; CAC36465.1; -;
 CC MIM: 605717; -;
 CC DR InterPro: IPR003599; Ig.
 CC DR InterPro: IPR003006; Ig_MHC.
 CC DR Pfam: PF00047; Ig; 2.
 CC DR SMART: SMO0409; Ig; 1.
 CC KW B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing.
 CC KW
 CC FT SIGNAL 1 18 POTENTIAL.
 CC FT CHAIN 19 302 ICOS LIGAND.
 CC FT DOMAIN 19 256 EXTRACELLULAR (POTENTIAL).
 CC FT TRASMEM 257 277 POTENTIAL.
 CC FT DOMAIN 278 302 CTOPPLASTIC (POTENTIAL).
 CC FT DOMAIN 30 120 IG-LIKE V-TYPE DOMAIN.
 CC FT DOMAIN 151 223 IG-LIKE C2-TYPE DOMAIN.
 CC FT DISULFID 37 113 POTENTIAL.

FT DISULFID 158 216 POTENTIAL.
 FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 173 173 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 225 225 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPLIC 300 302 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 302 AA; 33349 MM; 647934E21B55E34A CRC64;
 Query Match 9.4%; Score 147.5; DB 1; Length 302;
 Best Local Similarity 24.5%; Pred. No. 5.9e-05;
 Matches 66; Conservative 41; Mismatches 117; Indels 45; Gaps 13;
 QY 75 IGEDGILCTFEPPD---IKISDIYIOMKKGVLGVHEFREGDESEODEMFRGRTAVF 131
 DB 29 VGSDELVELSCAC-DEGRFEDINDYVYVWTSKSTVYTHIPQSSLENVDSRYRNRALMS 87
 QY 132 ADVYVGNASRLKKNQVLTADGTYKCIITSKRG-----NANLEKKTGA-FSMPEYVND 185
 DB 88 PAGMLRKDFSLRLEFNTVPQDEQKFC-LVLSQSLGFEQEVLSVETLVHVAANFSPVVSAP 146
 QY 186 YNASE--TLRCEAPRMFPQPTVYMASOVDOGANFSEVSTSPLENSENYTMKVSVLYN 243
 DB 147 HSPQDELTFTCTGINSYPRPNYWKNTDNLDOALQNDYVFLNMRGL-YDVVSYLRI 205
 QY 244 V-TINNTYSMEIEN-----DIAKATG-DI---KVTSEI---KRSHQLLNLSKAS 286
 DB 206 ARPTSVNIGCCIEENVLLQQLTVGSGQNDIGERDKITERPVSSTGKRNATWSILAVLCL 265
 QY 287 L-----CYSSFFALSMA LLP 301
 DB 266 LVVVAVAIGWCRDRCILQSHSYAGAMAVSP 294
 RESULT 8
 ID CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE T LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN) (CTLA-4 COUNTER-RECEPTOR B7.2) (B70) (FUN-1) (B063).
 GN CD86 OR CD28LG2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Boussiotis V.A., Ng J.W.,
 RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RT "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RT cell proliferation.";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RT "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79(1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RC TISSUE=Foreskin;
 RX MEDLINE=95351831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RT "Genomic organization of the gene coding for the costimulatory human
 RT B-lymphocyte antigen B7-2 (CD86).";
 RL Immunogenetics 42:85-89(1995).

RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.V., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RT "CD80 (B7) and CD86 (B7.1) provide similar costimulatory signals for T
 RT cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Grubben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Wakasa H., Tedder T.F.;
 RT "The B7-2 (B7.0) costimulatory molecule expressed by monocytes and
 RT activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS.
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
 CC MONOCYTES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD86 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd86.htm".
 CC -----
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 CC -----
 DR EMBL: L25259; AAB58389.1; -;
 DR EMBL: U04343; AAB03814.1; -;
 DR EMBL: U17722; AAA86473.1; -;
 DR EMBL: U17717; AAA86473.1; JOINED.
 DR EMBL: U17718; AAA86473.1; JOINED.
 DR EMBL: U17719; AAA86473.1; JOINED.
 DR EMBL: U17721; AAA86473.1; JOINED.
 DR MIM: 601020; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 23
 FT CHAIN 24 329
 FT DOMAIN 24 247
 FT TRANSMEM 248 268
 FT DOMAIN 269 329
 FT DOMAIN 33 117
 FT DOMAIN 149 225
 FT DISULFID 40 110
 FT DISULFID 157 218
 FT CARBOHYD 33 33
 FT CARBOHYD 47 47
 FT CARBOHYD 135 135
 FT CARBOHYD 146 146
 FT CARBOHYD 154 154
 FT CARBOHYD 177 177
 FT CARBOHYD 192 192
 FT CARBOHYD 213 213
 FT CONFLICT 27 27
 SQ SEQUENCE 329 AA; 37696 MW; 65D4F382689CFTD CRC64;

Query Match 9.4%; Score 147.5; DB 1; Length 329;
 Best Local Similarity 23.4%; Pred. No. 6,7e-05;
 Matches 67; Conservative 43; Mismatches 109; Indels 67; Gaps 13;
 QY 50 IALIGRIGSRHSITVTYVASAGNIGEDGILCTF--EPDKLSDIYIOWLKEGVGLV 107
 DB 12 ILFWAFILSLGAAPLKIQAIV-----FNETADLPQFANSSQNSSELVEFVQDQENL-VL 65
 QY 108 HEFKGDELSEQDEMERGRTAVFADVOYVGNASLRKLNQVLTAGYIKYIITSKGK- 166
 DB 66 NEVLGKREKFDVSHSKVWGRTSPDS-----SWTLRLNLIQIKDKGLQYCIHHRKPKFGM 120
 QY 167 ---NANLEYTGA-FSMPEV---NDYNASSEFLRCEAPRMPPOPTVWASQVDOGAN 217
 DB 121 IRIHOMSELVLANFSQPELIVPISNTIENYIT-NLTCSSIHGIFEP----- 166
 QY 218 FSEVNTSFEIENSVNTKV-----VSFLYNTI-----NNTYSMIEN 256
 DB 167 ---KKMSVLLRTKNSITFYDGINQSDQNTVELDYVSISSVSFPDVTSMWTFICILET 222
 QY 257 DIAATGDIKTESEIKR--RSHQLQNS---KASLYSSPFAISM 297
 DB 223 DKTRILSSPFSIELEDPPQPPDHPITWITAVLPVYICVMFCLILM 268
 RESULT 9
 CD86_RABIT STANDARD; PRT; 330 AA.
 ID CD86_RABIT
 AC P42071;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE B LYMPHOCYTE ACTIVATION ANTIGEN CD86 PRECURSOR (ACTIVATION B7-2
 DE ANTIGEN).
 GN CD86.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OC NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=B/J X CHB:HM;
 RX MEDLINE=95369849; PubMed=7642234;
 RA Isono T., Seto A.;
 RT "Cloning and sequencing of the rabbit gene encoding T-cell
 RT costimulatory molecules".
 RL Immunogenetics 42:217-220(1995).
 CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ANERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 CC ONE C2-LIKE AND ONE V-LIKE DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D49842; BAA06442.1; -;
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor.
 FT SIGNAL 1 22
 FT POTENTIAL.


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FT CHAIN 23 330 B LYMPHOCYTE ACTIVATION ANTIGEN CD86.
FT DOMAIN 23 247 POTENTIAL.
FT TRANSMEM 248 268 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 269 330 IG-LIKE V-TYPE DOMAIN.
FT DOMAIN 149 225 IG-LIKE C2-TYPE DOMAIN.
FT DISULFID 40 110 POTENTIAL.
FT CARBOHYD 157 218 POTENTIAL.
FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 192 192 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 213 213 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 330 AA; 37142 MW; 935CDB5C57E3BE1 CRC64;

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Query Match 9.4%; Score 147.5; DB 1; Length 330;
Best Local Similarity 24.0%; Pred. No. 6,7e-05;
Matches 59; Conservative 44; Mismatches 80; Indels 63; Gaps 11;

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QY 38 SIISITIIAGATATITGFIGISGRHSITVTVASAGNIGEDGILCTF--EPDIKISDIY 95
DB 12 TVEVMAILLSGASLRI-----QAYFNKTADLPQFTISQSRSISELV 54
QY 96 IOWLKEGVGLVHEFEKDESEDEMFRGAVADQYVGNASIRKLVOLTADGY 155
DB 55 VEFQDERL-VLELFLGRKKPDNPVKYIGRTSF--DQ---ESMWOLINVOIKKGYV 108
QY 156 KCIYISKSGK-----NANLEYTGA-FSMPEYVNDYNA---SSEILRCAPMPPOPTV 206
DB 109 QCVHHRGAKGLVPIYOMNSELVLANFOPETLITNSITRNSAINLTCSSVQGYDEPK 168
QY 207 VMASQVDGANGSEVSNSEFELSENVTMKV-----VSILVNTINTNTSCMIEN 256
DB 169 MF-----FLKTEENATEYDGVIEKSDONTVGLYNISISG--STFSD 209
QY 257 DIAKAT 262
DB 210 DIRNAT 215

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RESULT 10
MOG_HUMAN STANDARD: PRT: 247 AA.
AC Q16653: Q14855; Q13054; Q13055; Q92891; Q92892; Q92893; Q92894;
AC Q92895; Q93053; Q99605; Q00713; Q00714; Q00715;
DT 01-NOV-1997 (Rel. 35; Created)
DT 01-NOV-1997 (Rel. 35; Last sequence update)
DT 20-AUG-2001 (Rel. 40; Last annotation update)
DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
GN MOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-95310943; PubMed-7790876;
RA Hilton A.A., Slavin A.J., Hilton D.J., Bernard C.C.A.;
RT "Characterization of cDNA and genomic clones encoding human myelin
RT oligodendrocyte glycoprotein."
RL J. Neurochem. 65:309-318(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RX MEDLINE-95054056; PubMed-7964757;
RA Pham-Dinh D., Allingant B., Ruberg M., della Gaspera B.,
RA Nussbaum J.-L., Dautigny A.;
RT "Characterization and expression of the cDNA coding for the human
RT myelin/oligodendrocyte glycoprotein."

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RL J. Neurochem. 63:2353-2356(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-96015053; PubMed-8530032;
RA Roth M.-P., Malfroy L., Offer C., Sevin J., Enault G., Borot N.,
RA Pontarotti P., Coppin H.;
RT "The human myelin oligodendrocyte glycoprotein (MOG) gene: complete
RT nucleotide sequence and structural characterization."
RL Genomics 28:241-250(1995).
RN [4]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RX MEDLINE-96115584; PubMed-8666381;
RA Pham-Dinh D., della Gaspera B., de Rosbo N.K., Dautigny A.;
RT "Structure of the human myelin/oligodendrocyte glycoprotein gene and
RT multiple alternative spliced isoforms."
RL Genomics 29:345-352(1995).
RN [5]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RA Ballenthin P.A., Gardiner M.V.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [6]
RP STRUCTURE BY NMR OF 64-84.
RX MEDLINE-97354172; PubMed-9210466;
RA Albouze-Abou S., Wilson J.C., Bernard C.C.A., von Itzstein M.;
RT "A conformational study of the human and rat encephalitogenic myelin
RL oligodendrocyte glycoprotein peptides 35-55."
RL Eur. J. Biochem. 246:59-70(1997).
CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
CC COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
CC CELL COMMUNICATION.
CC -1- SUBUNIT: MAY FORM HOMO- OR HETERODIMERS BETWEEN THE DIFFERENT
CC ISOMERFORMS.
CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (ISOMERFORMS ALPHA-1
CC AND BETA-1); TYPE I MEMBRANE PROTEIN (OTHER ISOMERFORMS) (POTENTIAL).
CC -1- ALTERNATIVE PRODUCTS: AT LEAST 9 ISOMERFORMS: ALPHA-1 (SHOWN HERE),
CC -2-, -3-, -4, BETA-1, -2, -3, -4 AND A SHORT ISOMERFORM ARE PRODUCED BY
CC ALTERNATIVE SPLICING. THE SHORT ISOMERFORM IS NOT FUNCTIONALLY
CC ACTIVE. IT MAY BE EXPRESSED AT LOW LEVEL IN THE ADULT.
CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
CC LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
CC MEMBRANES.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE V-LIKE DOMAIN. BELONGS TO THE RTN/MOG SUPERFAMILY.
CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)
CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
CC -----
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CC -----
DR EMBL: X74511; CAA52617.1; -
DR EMBL: Z48051; CAA88109.1; -
DR EMBL: U18840; AAC50361.1; -
DR EMBL: U18843; AAC50362.1; -
DR EMBL: U18798; AAC50876.1; -
DR EMBL: U18799; AAC50877.1; -
DR EMBL: U18800; AAB36870.1; -
DR EMBL: U18801; AAC50878.1; -
DR EMBL: U18803; AAC50879.1; -
DR EMBL: U64564; AAB08088.1; -
DR EMBL: U64565; AAB08089.1; -
DR EMBL: U64566; AAB08090.1; -
DR EMBL: U64567; AAB08091.1; -
DR EMBL: U64568; AAB08092.1; -
DR EMBL: U64569; AAB08093.1; -
DR EMBL: U64570; AAB08094.1; -
DR EMBL: U64571; AAB08095.1; -
DR HSSP: O13740; 1KTC.
DR MIM: 159465; -.

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FT CARBOHYD 154 154 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 309 AA; 34665 MW; 8F58DCD1F81D5EA CRC64;

Query Match
 Best Local Similarity 22.6%; Pred. No. 0.00013;
 Matches 50; Conservative 53; Mismatches 83; Indels 35; Gaps 10;

QY 64 ITVTYVASSAGNT-----GEGDILSTCF--EPDIKLSDIVIOMLKEGVGLVHEFEKGD 115
 DB 15 VYLLLSADVAVETQAVFNGTAYLPQFTFAQINISSELVFVWQDQKL-VLEYHVLGTE 73
 QY 116 ELSEODEMFRGRTAVFADQVIVGNASLRKLVNLTAGTYKCIITISKGNANLEYK-- 173
 DB 74 KLDVNAKILGRTSF--DR---NNWTLRLHNVQIKDMGSDYDCKIQRKPPGSIILQOQTLL 128
 QY 174 ---TGAFSPMEVNVVDYNASSET---LRCEAPRFPQPTVYVNASQVQDQGANFSEVNTSP 226
 DB 129 ELSTVIANFSEPEIKLQANTGNGINLTCTSKQGHKPKKMYFLITNSTNEIGD---NM 184
 QY 227 ELNSEVNTKVVSVLYNVTI-----NNTYSCEMIENDIAK 260
 DB 185 QISQDNVT-ELFSISNSLSLSPFDGVMHMTVCVLETESMK 224

RESULT 12
 MOG_BOVIN
 ID MOG_BOVIN STANDARD; PRT; 246 AA.
 AC P55803;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.
 GN MOG.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 63-70.
 RC TISSUE=Brain;
 RX MEDLINE=93376728; PubMed=8367453;
 RA Pham-Dinh D., Mattei M.-G., Nussbaum J.-L., Roussel G.,
 Pontarotti P., Roedel N., Mather I.H., Artzt K., Lindahl K.F.,
 Dautigny A.;
 RT "Myelin/oligodendrocyte glycoprotein is a member of a subset of the
 immunoglobulin superfamily encoded within the major
 histocompatibility complex";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:7990-7994(1993).
 RL [2]
 RN SEQUENCE OF 29-36.
 RP TISSUE=Brain;
 RX MEDLINE=93382604; PubMed=8371836;
 RA Birling M.C., Roussel G., Nussbaum F., Nussbaum J.-L.;
 RT "Biochemical and immunohistochemical studies with specific polyclonal
 antibodies directed against bovine myelin/oligodendrocyte
 glycoprotein.";
 RT Neurochem. Res. 18:937-945(1993).
 CC -1- FUNCTION: MINOR COMPONENT OF THE MYELIN SHEATH. MAY BE INVOLVED IN
 COMPLETION AND/OR MAINTENANCE OF THE MYELIN SHEATH AND IN CELL-
 CELL COMMUNICATION.
 CC -1- SUBUNIT: MAY FORM HOMODIMERS.
 CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
 CC -1- TISSUE SPECIFICITY: FOUND EXCLUSIVELY IN THE CNS, WHERE IT IS
 LOCALIZED ON THE SURFACE OF MYELIN AND OLIGODENDROCYTE CYTOPLASMIC
 MEMBRANES.
 CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
 ONE V-LIKE DOMAIN. BELONGS TO THE RTN/MOG SUPERFAMILY.
 CC -1- CAUTION: DO NOT CONFUSE MYELIN-OLIGODENDROCYTE GLYCOPROTEIN (MOG)

CC WITH OLIGODENDROCYTE-MYELIN GLYCOPROTEIN (OMG).
 CC -----
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 CC -----
 DR EMBL: L21757; NOT_ANNOTATED_CDS.
 DR HSSP: Q13740; 1KJC.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00406; IgV; 1.
 KW Immunoglobulin domain; Glycoprotein; Myelin; Transmembrane; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 246
 FT DOMAIN 29 153 MYELIN-OLIGODENDROCYTE GLYCOPROTEIN.
 FT TRANSMEM 154 174 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 175 209 POTENTIAL.
 FT TRANSMEM 210 230 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 231 246 POTENTIAL.
 FT DOMAIN 246 246 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 45 133 IC-LIKE V-TYPE DOMAIN.
 FT DISULFID 52 126
 FT CARBOHYD 59 59
 SQ SEQUENCE 246 AA; 28028 MW; 363C76AB1A33DE41 CRC64;

Query Match
 Best Local Similarity 8.9%; Score 140.5; DB 1; Length 246;
 Matches 31; Conservative 25; Mismatches 50; Indels 13; Gaps 1;

QY 68 TVASAGN-----IGEDGILSTCFEPDIKLSDIVIOMLKEGVGLVHEFEKGD 114
 DB 24 TSSSAGQFRVIGRPHIRALVGDVEVLPGRISPKKATGMEGWIRPPRSRVVHLRNCK 83
 QY 115 ELSEODEMFRGRTAVFADQVIVGNASLRKLVNLTAGTYKCIITISKGNANLEYK 173
 DB 84 DODEGAPREYRGRTQLKETIGEGKVTLRIRNVRFSDGCGFCFPHDSYQDEAMELK 142

RESULT 13
 NCA2_HUMAN
 ID NCA2_HUMAN STANDARD; PRT; 761 AA.
 AC P13592; P13593;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE, PHOSPHATIDYLINOSITOL-LINKED ISOFORM
 GN PRECURSOR (N-CAM 120) (NCAM-120) (CD56 ANTIGEN).
 GN NCAM1 OR NCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (N-CAM 120).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=89305258; PubMed=3253057;
 RA Barton C.H., Dickson G., Gower H.J., Rowett L.H., Putt W.,
 Elsom V., Moore S.E., Goridis C., Walsh F.S.;
 RT "Complete sequence and in vitro expression of a tissue-specific
 phosphatidylinositol-linked N-CAM isoform from skeletal muscle";
 RT Development 104:165-173(1988).
 RL [2]
 RN SEQUENCE OF 491-761 FROM N.A. (N-CAM 120).
 RP TISSUE=Skeletal muscle;
 RX MEDLINE=87301755; PubMed=2887295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
 Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RT "Human muscle neural cell adhesion molecule (N-CAM): identification

RT of a muscle-specific sequence in the extracellular domain."
 RL Cell 50:1119-1130(1987).
 RN [3]
 RP SEQUENCE OF 491-655 FROM N.A. (SECRETED ISOFORM).
 RX MEDLINE=9077552; PubMed=3203385;
 RA Gower H.J., Barton C.H., Elsom V.L., Thompson J., Moore S.E.,
 RA Dickson G., Walsh F.S.;
 RT "Alternative splicing generates a secreted form of N-CAM in muscle
 and brain".
 RL Cell 55:955-964(1988).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROM; NOTE-CD guide CD56 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd56.htm".
 CC -----
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 CC -----
 CC EMBL: X16841; CAA34739.1; -
 CC EMBL: M17409; AAA59912.1; -
 CC EMBL: M22094; AAA59910.1; -
 CC EMBL: M22092; AAA59911.1; -
 CC EMBL: M22091; AAA59911.1; JOINED.
 CC PIR: S07784; IJHUNG.
 CC PIR: A31635; A31635.
 CC MIM: 116930; -
 CC InterPro: IPR001777; FN.III.
 CC InterPro: IPR003006; IG.MHC.
 CC InterPro: IPR003598; IG.C2.
 CC Pfam: PF00041; Fn3; 2.
 CC Pfam: PF00047; Ig; 5.
 CC SMART: SM00060; FN3; 2.
 CC SMART: SM00408; IGc2; 5.
 CC KW Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 CC GPI-anchor; Alternative splicing.
 CC FT SIGNAL 1 19
 CC FT CHAIN 20 761
 CC FT
 CC FT DOMAIN 34 103 NEURAL CELL ADHESION MOLECULE,
 CC FT DOMAIN 132 196 PHOSPHATIDYLINOSITOL-LINKED ISOFORM.
 CC FT DOMAIN 228 294 IG-LIKE C2-TYPE DOMAIN 1.
 CC FT DOMAIN 322 392 IG-LIKE C2-TYPE DOMAIN 2.
 CC FT DOMAIN 419 486 IG-LIKE C2-TYPE DOMAIN 3.
 CC FT DOMAIN 518 595 IG-LIKE C2-TYPE DOMAIN 4.
 CC FT DOMAIN 660 727 FIBRONECTIN TYPE-III 1.
 CC FT DISULFID 41 96 FIBRONECTIN TYPE-III 2.
 CC FT DISULFID 139 189 PROBABLE.
 CC FT DISULFID 235 287 PROBABLE.
 CC FT DISULFID 329 385 PROBABLE.
 CC FT DISULFID 426 479 PROBABLE.
 CC FT CARBOHYD 222 222 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 347 347 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 423 423 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 449 449 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT CARBOHYD 478 478 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC FT VARSPLIC 635 655 GEPSAPLECGMGEDGNSIV -> NIAOHCCNMCQAGLH
 CC FT NALMK (IN SECRETED ISOFORM).
 CC FT SEQUENCE 761 AA; 83770 MW; F0CAD3292D7AB67E CRC64;
 CC

Query Match

8.6%; Score 135; DB 1; Length 761;

Best Local Similarity 23.2%; Pred. No. 0.0022;
 Matches 64; Conservative 49; Mismatches 11; Indels 52; Gaps 13;
 QY 63 SIYTVYASAGNIGEDGILSTF-----EPDILSDIYIOWLKEGYGLVHEKEGDE 116
 Db 77 SSSYTLTYNA-NIDDAIGYKCVYGEDGSESEATVNVKIFQKLMFKNAPPPQEFREGEDA 135
 QY 117 LSEDDK-----FRGTAVFAQV---YGNASLRKNNVOLDAGYKCYITSK 163
 Db 136 VIVCDVVSLEPTTIKHKAGDYILKQVREIVTSNNYLOIGIKTDEGYRC-----E 190
 QY 164 G-----KGNANLEYTKGAFSPE-----VNVDYN-ASSETLRCAPRPFPTVYVAS 210
 Db 191 GRIARBEINPKDQIVYVNPPTIQARQNIYVATNANLGQSTLYVCA-EGSPPEPTMGWK 249
 QY 211 QVDGANGFSEVSNTPSELSNENYTKVSVLYVNTYNTYSCMIENDIAK--ATGDIKYT 268
 Db 250 DGEIEDEDEDEKIFSDSSQTLIKRV---DKNDEAEYICIAENKAGEDATIHKVF 305
 QY 269 E-----SEIKRSHQLNKSASLCVSS---FFAISW 297
 Db 306 AKPRITVVENOTAMELEBYTLTCEASGDPIPSITW 341
 RESULT 14
 NCAL_HUMAN STANDARD; PRT; 848 AA.
 AC P13591; Q16180; Q15829;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
 DE (NCAM-140) (CD56 ANTIGEN).
 GN NCAM1 OR NCAM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94356433; PubMed=80759973;
 RA Saito S., Tani Y., Tachibana I., Hayashi S., Kishimoto T., Kawase I.;
 RT "Complementary DNA sequence encoding the major neural cell adhesion
 RT molecule isoform in a human small cell lung cancer cell line.";
 RL Lung Cancer 10:307-318(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91250739; PubMed=1710251;
 RA Lanier L.L., Chang C., Azuma M., Rutenberg J.J., Hemperly J.J.,
 RA Phillips J.H.;
 RT "Molecular and functional analysis of human natural killer cell-
 RT associated neural cell adhesion molecule (N-CAM/CD56)."
 RL J. Immunol. 146:4421-4426(1991).
 RN [3]
 RP SEQUENCE OF 491-848 FROM N.A.
 RX MEDLINE=87301755; PubMed=2887295;
 RA Dickson G., Gower H.J., Barton C.H., Prentice H.M., Elsom V.L.,
 RA Moore S.E., Cox R.D., Quinn C., Putt W., Walsh F.S.;
 RT "Human muscle neural cell adhesion molecule (N-CAM): identification
 RT of a muscle-specific sequence in the extracellular domain".
 RL Cell 50:1119-1130(1987).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- DATABASE: NAME-PROM; NOTE-CD guide CD56 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd56.htm".
 CC -----
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DR EMBL: S71824; AAB31836.1; -
 DR EMBL: U63041; AAB04558.1; -
 DR EMBL: M17410; AAA59913.1; -
 DR PIR: B26883; B26883.
 DR MIM: 116930; -
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00060; FN3; 2.
 DR SMART: SM00408; IGc2; 5.
 DR Immunoglobulin domain; Cell adhesion; Glycoprotein; Repeat; Signal;
 KW Transmembrane; Alternative splicing.
 FT SIGNAL 1 19
 FT CHAIN 20 848
 FT DOMAIN 20 708
 FT TRANSMEM 709 729
 FT DOMAIN 730 848
 FT DOMAIN 34 103
 FT DOMAIN 132 196
 FT DOMAIN 228 294
 FT DOMAIN 322 392
 FT DOMAIN 419 486
 FT DOMAIN 518 595
 FT DOMAIN 660 727
 FT DISULFID 41 96
 FT DISULFID 139 189
 FT DISULFID 235 287
 FT DISULFID 329 385
 FT DISULFID 426 479
 FT CARBOHYD 222 222
 FT CARBOHYD 315 315
 FT CARBOHYD 347 347
 FT CARBOHYD 423 423
 FT CARBOHYD 449 449
 FT CARBOHYD 478 478
 FT CONFLICT 215 215
 FT CONFLICT 239 239
 FT CONFLICT 490 490
 FT CONFLICT 599 600
 FT CONFLICT 720 721
 FT CONFLICT 811 811
 SO SEQUENCE 848 AA; 93360 MW; 68D2F0C0E6C1C2AD CRC64;

Query Match 8.6%; Score 135; DB 1; Length 848;
 Best Local Similarity 23.2%; Pred. No. 0.0026;
 Matches 64; Conservative 49; Mismatches 111; Indels 52; Gaps 13;

QY 63 SITVTYASAGNIGEDGLSTF-----EPDIKSDIVIQWLEGLVGLVHERKEGDE 116
 DB 77 SSSLTITLYNA-NIDDAIGYKCVTGEDSESEATVNVKIFQKLMFNKAPFOEPFREGDA 135
 QY 117 LSEODEM-----FRGRTAVFADQY---IYGNASLRKKNQVLDAGYKCYITTSK 163
 DB 136 VIVCDVVSLEPTTIWKHKGDVILIKKDVRIIVSNNTLQIRGIKKKDEGTIRC-----E 190
 QY 164 G-----KGNANLEYKTGAFSME-----VNVQYN-ASSETLCEAPRMPPOPTVVAS 210
 DB 191 GRIIARGLINKDQVIVNVPTIOANQNTVMAFANAGOSTLVCDAA-EGEPETPMSTK 249
 QY 211 QVQDGANSEVSNSTSEFELSENVTMKVSVLYNVTINNYSCTMIENDIAK--AAGDIKVT 268
 DB 250 DGEIOEEDDEDEKXIFSDSSQLTIKKV----DKNDEAYICIAENKAGDEDAIHLKVF 305

QY 269 E-----SEIKRRSHLQILNSKASICVSS---FPAISW 297
 DB 306 AKRKITYVENQTMAMELEQVTLTCEASGDPISITW 341

RESULT 15
 ID NCAL_BOVIN STANDARD; PRT; 853 AA.
 AC P31836;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE NEURAL CELL ADHESION MOLECULE, 140 KDA ISOFORM PRECURSOR (N-CAM 140)
 DE (NCAM-140).
 GN NCAM1 OR NCAM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Brain cortex;
 RX MEDLINE=89378239; PubMed=2776887;
 RA Lipkin V.M., Khramtsov N.V., Andreeva S.G., Moshnyakov M.V.,
 RA Petukhova G.V., Rakitina T.V., Feshchenko E.A., Ishchenko K.A.,
 RA Mirzoeva S.F., Chernova M.N., Dranyatsyna S.M.;
 RT "Calmodulin-independent bovine brain adenylate cyclase. Amino acid
 RT sequence and nucleotide sequence of the corresponding cDNA.";
 RL FEBS Lett. 254:65-73(1989).
 RN [2]
 RP SEQUENCE OF 20-36.
 RX MEDLINE=86140120; PubMed=3512556;
 RA Rougon G., Marshak D.R.;
 RT "Structural and immunological characterization of the amino-terminal
 RT domain of mammalian neural cell adhesion molecules.";
 RL J. Biol. Chem. 261:3396-3401(1986).
 RN [3]
 RP IDENTIFICATION AS N-CAM.
 RX MEDLINE=92111748; PubMed=1765159;
 RA Premont R.T.;
 RT "A bovine brain cDNA purported to encode calmodulin-insensitive
 RT adenylate cyclase has extensive identity with neural cell adhesion
 RT molecules (N-CAMs).";
 RL FEBS Lett. 295:230-231(1991).
 CC -1- FUNCTION: THIS PROTEIN IS A CELL ADHESION MOLECULE INVOLVED IN
 CC NEURON-NEURON ADHESION, NEURITE FASCICULATION, OUTGROWTH OF
 CC NEURITES, ETC.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- ALTERNATIVE PRODUCTS: THE DIFFERENT TISSUE-SPECIFIC FORMS OF
 CC N-CAM ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- SIMILARITY: CONTAINS 5 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- CAUTION: WAS ORIGINALLY (REF.1) THOUGHT TO BE A CALMODULIN-
 CC INDEPENDENT ADENYLATE CYCLASE.

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DR EMBL: X16451; CAA34470.1; -
 DR PIR: A32976; IBONC.
 DR HSSP: P40189; IBQU.
 DR InterPro: IPR001777; FN_III.
 DR InterPro: IPR003006; IG_MHC.
 DR InterPro: IPR003598; IG_c2.
 DR Pfam: PF00041; fn3; 2.
 DR Pfam: PF00047; Ig; 5.

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